

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 13, 2006, 13:40:22 ; Search time 194 Seconds  
(without alignments)  
723.533 Million cell updates/sec

Title: US-10-510-941-2  
Perfect score: 1542  
Sequence: 1 LETLLKKNVSKTIRGKKII.....KSLDRFLFETADKERAQHV 307

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8.\*

- 1: Geneseq1980s.\*
- 2: Geneseq1950s.\*
- 3: Geneseq2000s.\*
- 4: Geneseq2001s.\*
- 5: Geneseq2002s.\*
- 6: Geneseq2003as.\*
- 7: Geneseq2003bs.\*
- 8: Geneseq2004s.\*
- 9: Geneseq2005s.\*
- 10: Geneseq2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1542	100.0	307	7	ADN97355 B. lichen
2	738.5	47.9	310	8	ADS27585 Bacterial
3	734	47.6	301	5	ABBA47477 Listeria
4	734	47.6	301	6	ABU32480 Protein e
5	639	41.4	306	5	ABBA48180 Listeria
6	638	41.4	309	8	ADG32114 Mutant B
7	536	34.8	302	6	ABU44428 Protein e
8	535.5	34.7	306	8	ADS28089 Bacterial
9	516	33.5	299	8	ADN27185 Bacterial
10	501	32.5	311	8	ADN48041 Thermococ
11	493	32.0	306	8	ADS41933 Bacterial
12	493	32.0	308	8	ADN18644 Bacterial
13	491.5	31.9	308	8	ADN18683 Bacterial
14	490	31.8	309	8	ADN46530 Thermococ
15	485	31.5	221	8	ADS27537 Bacterial
16	484.5	31.4	308	10	ABE95518 E. faecali
17	474.5	30.8	322	8	ADN46418 Thermococ
18	473	30.7	305	4	ABB96628 Putative
19	473	30.7	305	8	ADS43172 Bacterial
20	455.5	29.5	306	6	ABU25506 Protein e
21	455.5	29.5	310	7	ADC97283 E. faeciu
22	451.5	29.3	325	4	ABB96710 Putative
23	451	29.2	300	5	ABP26280 Streptoco

24	447.5	29.0	285	6	ABU26098 Protein e
25	447.5	29.0	377	6	ADN11670 Alloiococ
26	444	28.8	328	8	ADN46668 Thermococ
27	442	28.7	300	5	ABP26335 Streptoco
28	442	28.7	300	8	ADV88530 Streptoco
29	442	28.7	300	8	ADV81939 Streptoco
30	442	28.7	300	8	ADV79783 Streptoco
31	438	28.4	311	8	ADS22213 Bacterial
32	436	28.3	233	5	ABB09645 Amino aci
33	436	28.3	233	6	ABG72543 Streptoco
34	436	28.3	233	8	ADU80820 MutF, SEQ
35	435.5	28.2	297	8	ADS29173 Bacterial
36	434.5	28.2	305	8	ADN47270 Thermococ
37	432.5	28.0	310	6	ABU24420 Protein e
38	431.5	28.0	305	8	ADS29082 Bacterial
39	431.5	28.0	316	8	ADS29721 Bacterial
40	430.5	27.9	233	8	ADS22132 Bacterial
41	430.5	27.9	332	7	ADC94125 E. faeciu
42	429	27.8	312	4	AAG92767 C glutami
43	428.5	27.8	306	8	ADN46278 Thermococ
44	425	27.6	308	8	ADS27622 Bacterial
45	424.5	27.5	312	8	ADN18549 Bacterial

## ALIGNMENTS

RESULT 1  
ADN97355  
ID ADN97355 standard; protein; 307 AA.  
XX AC ADN97355;  
XX AC ADN97355;  
DT 01-JUL-2004 (first entry)  
XX B. licheniformis antibiotic synthesis related protein SEQ ID NO:2.  
DE antibiotic synthesis; proteolytic; protease.  
KW Bacillus licheniformis.  
XX WO2003087142-A2.  
XX 23-OCT-2003.  
XX 25-MAR-2003; 2003WO-DK000199.  
XX 10-APR-2002; 2002DK-00000532.  
XX (NOVO ) NOVOZYMES AS.  
XX Andersen JT, Jorgensen ST, Raemussen MD, Olsen PB, Clausen IG;  
WPI; 2003-833704/77.  
XX N-PSDB; ADN97354.  
XX New Bacillus licheniformis mutant host cell that is mutated in one or  
more gene(s) encoding one or more polypeptide(s) having proteolytic  
activity, useful for producing, isolating and/or purifying at least one  
product of interest.  
XX Disclosure; SEQ ID NO 2; 100pp; English.  
XX The invention relates to a novel Bacillus licheniformis mutant host cell  
derived from a parent B. licheniformis host cell, where the mutant host  
cell is mutated in one or more gene(s) encoding one or more  
polypeptide(s) having proteolytic activity that is at least 80% identical  
to any of the 22 amino acid sequences fully defined in the specification,  
where the mutant host cell expresses at least 5% less of one or more  
polypeptide(s) having a proteolytic activity than the parent host cell,  
when they are cultivated under comparable conditions. The host cell is  
useful for producing at least one product of interest, and for isolating  
or purifying the product of interest. The present sequence represents an

*[Handwritten signature]*

CC antibiotic synthesis related polypeptide of the invention.

XX Sequence 307 AA;

Query Match 100.0%; Score 1542; DB 7; Length 307;  
Best Local Similarity 100.0%; Pred. No. 3e-130;  
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LETLLEKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGAGKTTTIRMIVGHMSTAGE 60  
DB 1 LETLLEKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGAGKTTTIRMIVGHMSTAGE 60  
QY 61 IAVCGSVKENFEKAAARHIGAIIVENPELYKFLTYGQNLQOYARMTKGVTKKKIDEIVELV 120  
DB 61 IAVCGSVKENFEKAAARHIGAIIVENPELYKFLTYGQNLQOYARMTKGVTKKKIDEIVELV 120  
QY 121 GLKNRINDKVYSLGMRORGLAQSLLDHPKLLIIDEPTNGLDPAIGIREIRDYLRKLT 180  
DB 121 GLKNRINDKVYSLGMRORGLAQSLLDHPKLLIIDEPTNGLDPAIGIREIRDYLRKLT 180  
QY 181 EKGMAVIVSHLLSEMELMCDRTAIIONGKLDIQHVHGPARDKKRYIQADDTQALTR 240  
DB 181 EKGMAVIVSHLLSEMELMCDRTAIIONGKLDIQHVHGPARDKKRYIQADDTQALTR 240  
QY 241 EAAAFKRVKVDAAEGGIELSIQKDEVPDLIKHLTDSGVRLYEYKAVNKSLEDRFLITAD 300  
DB 241 EAAAFKRVKVDAAEGGIELSIQKDEVPDLIKHLTDSGVRLYEYKAVNKSLEDRFLITAD 300  
QY 301 KEEAQHV 307  
DB 301 KEEAQHV 307

# RESULT 2

ADSD27585 standard; protein; 310 AA.

XX ADSD27585;

XX 02-DEC-2004 (first entry)

XX Bacterial polypeptide #16618.

DE Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.

XX Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.  
XX (HINK/) HINKLE G J.  
XX (SLAT/) SLATER S C.  
XX (CHEN/) CHEN X.  
XX (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide  
PT for expression of a polynucleotide encoding a polypeptide from a

PT microbial source, useful for producing plants with improved properties.  
XX Claim 1; SEQ ID NO 16618; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition, improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

XX Sequence 310 AA;

Query Match 47.9%; Score 738.5; DB 8; Length 310;

Best Local Similarity 48.5%; Pred. No. 7.8e-58;

Matches 147; Conservative 66; Mismatches 81; Indels 9; Gaps 3;

QY 1 LETLLEKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGAGKTTTIRMIVGHMSTAGE 60  
DB 10 MTTILSVRLDKKVIIGKTLIVENISPDVKQGEVFGFLGPNAGAGKTTTIRMIVGLIKATEGT 69  
QY 61 IAVCGSVKENFEKAAARHIGAIIVENPELYKFLTYGQNLQOYARMTKGVTKKKIDEIVELV 120  
DB 70 ISIGYSIKENFREAMRQIGSIVENPELYTTLTGWENLAKQFARMGLGDISERIEIAEMV 129  
QY 121 GLKNRINDKVYSLGMRORGLAQSLLDHPKLLIIDEPTNGLDPAIGIREIRDYLRKLT 180  
DB 130 HLDERIHDKVKTYSYLGMRORGLAQSLLDHPKLLIIDEPTNGLDPAIGIREIRDYLRKLT 189  
QY 181 EKGMAVIVSHLLSEMELMCDRTAIIONGKLDIQHVHGPARDKKRYIQADDTQOA 237  
DB 190 EENMSVFISSHLLSEVQMICDRVAIIHKGMITVAKVEELIKTASDRVEHIVTPISKAKD 249  
QY 238 LTREAAAFKRVKVDAAEGGIELSIQKDEVPDLIKHLTDSGVRLYEYKAVNKSLEDRFL 295  
DB 250 MLEAAKEVREVSVE----GDRLLCRMDIASISSWNKHFVENEIDVHVKELVFTLEDLFI 305  
QY 296 EIT 298  
DB 306 ELT 308

# RESULT 3

ABB47477

ID ABB47477 standard; protein; 301 AA.

XX ABB47477;

XX 05-FEB-2002 (first entry)

XX Listeria monocytogenes protein #181.

XX Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;  
KW vitamin B12; bacterial infection; disease.

OS Listeria monocytogenes.

XX WO200177335-A2.  
XX 18-OCT-2001.  
XX PF 11-APR-2001; 2001WO-FR001118.  
XX PR 11-APR-2000; 2000FR-00004629.  
XX PA (INSP ) INST PASTEUR.  
XX

XX Buchrieser C, Frangeul L, Couve E, Rusniok C, Felhi H, Dehoux P;  
PI Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;  
PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;  
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;  
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;  
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;  
PI Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;  
PI Rose M, Voss H;  
XX  
XX WPI; 2002-010914/01.  
XX

XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment  
PT and prevention of Listeria and related bacterial infections, and related  
PT polypeptides.  
XX

XX Claim 6; SEQ ID NO 182; 192pp; French.

XX The present invention relates to the genome sequence of Listeria  
CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of  
CC it are useful for selecting probes and primers for detecting genes in L.  
CC monocytogenes and related organisms, and for studying genetic  
CC polymorphisms and other genomes. The present sequence is a protein  
CC encoded by the genome sequence of the present invention. Proteins  
CC expressed from the genome sequence are useful for raising specific  
CC antibodies, identification of L. monocytogenes and related organisms, and  
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin  
CC B12. The genome sequence and proteins encoded by it are also useful for  
CC selecting compounds that regulate gene expression and cell replication  
CC and modulate L. monocytogenes-related diseases. In addition, the genome  
CC sequence and proteins encoded by it are useful in pharmaceutical and  
CC vaccine compositions for the treatment or prevention of infections by L.  
CC monocytogenes and related organisms. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX

SQ Sequence 301 AA;

Query Match 47.6%; Score 734; DB 5; Length 301;  
Best Local Similarity 49.8%; Pred. No. 1.9e-57;  
Matches 149; Conservative 61; Mismatches 81; Indels 8; Gaps 3;  
QY 2 ETLELKNVSKTRGKKGITGLSFDVRAGBIFGLPNGAGKTTTIRMIVGHMSITAGEI 61  
DB 3 ERALQVTLNHLKTKREILNGISFVWMPGEVDFGLPNGAGKTTTIRMIVGLIKPSTGII 62  
QY 62 AVCGSVKNEFKAARHGAIVENPELYKFLTCYQNLQOYARMTKGVTKKIDIEIVELVG 121  
DB 63 LIGGKDIRKNFTAMRGLSGSIVENPEFYTLTQENLAVFARMDSIIKKERIQEVTELVG 122  
QY 122 LKQRINDKVTYSLGNRORLGLAOSLLHDPKLLILDEPTNGLDPAGIRETRVLRKLTRE 181  
DB 123 LKQRINDRSTVSLGNRQRLGIAQALLSNPKLLILDEPTNGLDPSGIHEMRDFIRALARN 182  
QY 182 KGMNVSVSHLSEMLMCDRIAIIONGK-LRDIQHVHGPARDEKKRYITQADDTQALTR 240  
DB 183 EGISLVSSHLSLSEIELLDCRVAIMTDGTITKTDQVAHLLSSRAQLRWVTP-----LE 236  
QY 241 EAAAF-RKKVDPBAEGGIELSIQKDEVPDLIKHLTDSGVRLVYEVKAVNKSLEDRFLEIT 298  
DB 237 QAKAFLESVTEVDEYLVLTAMNEESAENWQNLVAKGIKWHIDKRPKSPLEDFLELT 295

RESULT 4  
ABU32480  
ID ABU32480 standard; protein; 301 AA.  
XX AC ABU32480;  
XX DT 19-JUN-2003 (first entry)  
XX DE Protein encoded by Prokaryotic essential gene #18007.  
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX OS Listeria monocytogenes.  
XX PN WO200277183-A2.  
XX PD 03-OCT-2002.  
XX PF 21-MAR-2002; 2002WO-US009107.  
XX PR 21-MAR-2001; 2001US-00815242.  
XX PR 06-SEP-2001; 2001US-00948993.  
XX PR 25-OCT-2001; 2001US-0342923P.  
XX PR 08-FEB-2002; 2002US-00072851.  
XX PR 06-MAR-2002; 2002US-0362899P.  
XX PA (ELIT-) ELITRA PHARM INC.  
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;  
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX WPI; 2003-029926/02.  
XX N-PSDB; ACA36350.  
XX New antisense nucleic acids, useful for identifying proteins or screening  
PT for homologous nucleic acids required for cellular proliferation to  
PT isolate candidate molecules for rational drug discovery programs.  
XX Claim 25; SEQ ID NO 60404; 1766pp; English.  
XX The invention relates to an isolated nucleic acid comprising any one of  
CC the 6213 antisense sequences given in the specification where expression  
CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
CC (1) a vector comprising a promoter operably linked to the nucleic acid  
CC encoding a polypeptide whose expression is inhibited by the antisense  
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
CC polypeptide or its fragment whose expression is inhibited by the  
CC antisense nucleic acid; (4) an antibody capable of specifically binding  
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
CC proliferation or the activity of a gene in an operon required for  
CC proliferation; (7) identifying a compound that influences the activity of  
CC the gene product or that has an activity against a biological pathway  
CC required for proliferation, or that inhibits cellular proliferation; (8)  
CC identifying a gene required for cellular proliferation or the biological  
CC pathway in which a proliferation-required gene or its gene product lies  
CC on a gene on which the test compound that inhibits proliferation of an  
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
CC compound's activity; (11) a culture comprising strains in which the gene  
CC product is overexpressed or underexpressed; (12) determining the extent  
CC to which each of the strains is present in a culture or collection of  
CC strains; or (13) identifying the target of a compound that inhibits the  
CC proliferation of an organism. The antisense nucleic acids are useful for  
CC identifying proteins or screening for homologous nucleic acids required  
CC for cellular proliferation to isolate candidate molecules for rational  
CC drug discovery programs, or for screening homologous nucleic acids  
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
CC the target prokaryotic essential genes. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

```

XX Sequence 301 AA;
SQ
Query Match 47.6%; Score 734; DB 6; Length 301;
Best Local Similarity 49.8%; Pred. No. 1.9e-57;
Matches 149; Conservative 61; Mismatches 81; Indels 8; Gaps 3;

QY 2 ETLLEKNVSKTIRGKIIIEGLSFDVRAGEIFGLGPNAGKTTTIRMIVGHMSITAGEI 61
DB 3 ERALQVNLHKKIRKEIKIGISFVWPGVEVFGFGLGPNAGKTTTIRMIVGLIKPSTGI 62

QY 62 AVCGSVSKENFEKAAHIGAIIVENPELYKFLTYQNLQOYARMKGVTKKKIDEIVELVG 121
DB 63 LIGGKDIRKNFTAMRGLSGIVENPEFYTLTGQENLAVFARMSSIKKRIQEVTELVG 122

QY 122 LKRNINDKVTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTRE 181
DB 123 LKXRNDRVSTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTRE 182

QY 182 KGMVIVSSHLLSEMELMCDRIATIQNGK-LRDIQHVHGPARDKRYIYQADDTQALTR 240
DB 183 EGISVLVSSHLLSEIELLDCRVAIMTDTGIKTDOVAHLLSSRAQLRWVTP-----IS 236

QY 241 EAAAF-RKKVDRAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLEIT 298
DB 237 QAKAFLESVTEVEVDGELYVTANNEESAENWQNLVAKGIKVHBIIDKKRPSLEDFLEIT 295

RESULT 5
ABB48180
ID ABB48180 standard; protein; 306 AA.
XX
AC ABB48180;
XX
DT 05-FEB-2002 (first entry)
XX
DE Listeria monocytogenes protein #884.
XX
KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
KW vitamin B12; bacterial infection; disease.
XX
OS Listeria monocytogenes.
XX
PN WO200177335-A2.
XX
PD 18-OCT-2001.
XX
PF 11-APR-2001; 2001WO-FR001118.
XX
PR 11-APR-2000; 2000FR-00004629.
XX
PA (INSP ) INST PASTEUR.
XX
PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Feihi H, Dehoux P;
PI Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
PI Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
PI Chakraborty T, Donnann E, Hain T, Berche P, Charbit A, Durant L;
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
PI Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
PI Rose M, Voss H;
XX
XX WPI; 2002-010914/01.
XX
XX Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
XX and prevention of Listeria and related bacterial infections, and related
XX polypeptides.
XX
XX Claim 6; SEQ ID NO 885; 192pp; French.
XX
XX The present invention relates to the genome sequence of Listeria
XX monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
XX it are useful for selecting probes and primers for detecting genes in L.

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CC monocytogenes and related organisms, and for studying genetic
CC polymorphisms and other genomes. The present sequence is a protein
CC encoded by the genome sequence of the present invention. Proteins
CC expressed from the genome sequence are useful for raising specific
CC antibodies, identification of L. monocytogenes and related organisms, and
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate L. monocytogenes-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccine compositions for the treatment or prevention of infections by L.
CC monocytogenes and related organisms. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 306 AA;
Query Match 41.4%; Score 639; DB 5; Length 306;
Best Local Similarity 45.3%; Pred. No. 7.1e-49;
Matches 135; Conservative 57; Mismatches 104; Indels 2; Gaps 2;

QY 2 ETLLEKNVSKTIRGKIIIEGLSFDVRAGEIFGLGPNAGKTTTIRMIVGHMSITAGEI 61
DB 3 ETVLKHVTKIKIGKNIVHDSFIDHKGEVFGFGLGPNAGKTTTIRSIIVGLIRSEGTV 62

QY 62 AVCGSVSKENFEKAAHIGAIIVENPELYKFLTYQNLQOYARMKGVTKKKIDEIVELV 120
DB 63 FINGKNVDTEYKAAISEVCAIIEPEFYMYSGWANLKQFARMSQKNITDEHIREIVELV 122

QY 121 GLKRNINDKVTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLT 180
DB 123 KLTGAINQKVTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLT 181

QY 181 EKGMAVIVSSHLLSEMELMCDRIATIQNGKLRDIQHVHGPARDKRYIYQADDTQALTR 240
DB 182 TNGTSVLISLHLLSEIQITDRFALLINKGVLTIEKMSDLIENHVAAYKLVSDPVATTT 241

QY 241 EAAAFKRVKVDRAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLEIT 298
DB 242 VLATLPVKLVQNEDLFKIEVAHEDVHLIARALIQANIDLELVPLQASLEERFLEIT 299

RESULT 6
ADG32114
ID ADG32114 standard; protein; 309 AA.
XX
AC ADG32114;
XX
DT 26-FEB-2004 (first entry)
XX
DE Mutant B_licheniformis secreted polypeptide SeqID 84.
XX
KW mutant; host cell; production yield; shelf life; product stability;
KW purity; secreted; mutein.
XX
OS Synthetic.
XX Bacillus licheniformis.
XX
XX WO2003093453-A2.
XX
XX 13-NOV-2003.
XX
XX 25-MAR-2003; 2003WO-DK000198.
XX
XX 10-APR-2002; 2002DK-00000534.
XX
XX (NOVO ) NOVOZYMES AS.
XX
XX Andersen JT, Jorgensen ST, Rasmussen MD, Olsen PB, Clausen IG;
XX WPI; 2004-053045/05.
XX N-PSDB; ADG32113.

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Db 241 MRKGFEEBNSQIVLKDYNKNTIAAAVKVLVANDIIDYQVRMVRKSLEEVFLDMT 295

RESULT 8

ADS28089

ID ADS28089 standard; protein; 306 AA.

XX ADS28089;

AC

AD 02-DEC-2004 (first entry)

XX Bacterial polypeptide #17122.

XX Recombinant DNA construct; transformed plant; improved plant property;

KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;

KW pathogen tolerance; pest tolerance; plant disease resistance;

KW cell cycle pathway modification; plant growth regulator;

KW homologous recombination; seed oil yield; protein yield; carbohydrate;

KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

XX bacterial polypeptide.

XX Bacteria.

OS US2003233675-A1.

PN 18-DEC-2003.

PD 20-FEB-2003; 2003US-00369493.

PF 21-FEB-2002; 2002US-0360039P.

PR (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

PI WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide

PT for expression of a polynucleotide encoding a polypeptide from a

PT microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 17122; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a

CC promoter functional in a plant cell, where the promoter is positioned to

CC provide for expression of a polynucleotide encoding a polypeptide from a

CC microbial source. The invention also relates to a transformed plant

CC comprising the recombinant DNA construct and a method of producing a

CC transformed plant having an improved property. The plant is a crop plant

CC such as maize or soybean. The method of producing a transformed plant

CC having an improved property comprises transforming a plant with the

CC recombinant DNA construct and growing the transformed plant, where the

CC polynucleotide or polypeptide is useful for improving plant properties.

CC The recombinant DNA construct is useful for producing plants with

CC improved plant properties, e.g. improved cold, heat or drought tolerance,

CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,

CC increased resistance to plant disease, better growth rate by modification

CC of the cell cycle pathway with plant growth regulators, increased rate of

CC homologous recombination, modified seed oil or protein yield and/or

CC content, improved yield by modification of carbohydrate, nitrogen or

CC phosphorus use and/or uptake, by modification of photosynthesis or by

CC providing improved plant growth and development under at least one stress

CC condition, improved lignin production or improved galactomannan

CC production. This sequence represents a bacterial polypeptide used in the

CC scope of the invention. Note: The sequence data for this patent did not

CC form part of the printed specification but was obtained in electronic

CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

XX Sequence 306 AA;

Query Match 34.7%; Score 535.5; DB 8; Length 306;

Best Local Similarity 38.5%; Pred. No. 1.5e-39;

Matches 115; Conservative 69; Mismatches 106; Indels 9; Gaps 4;

QY 4 LLELKNVSKTIRGKKIIEGLSFDVRAGIFGFLGPNAGAGKTTTIRMIVGHMSITAGEIAV 63

Db 7 LIETNLTWYKHVAVDRINLKVKEGIYGLFPGNAGKTTTIRMLLGLIKASHGSIKI 66

QY 64 CGSVKENFEKAAARHIGAIVENPELYKFLTGYQNIQQVARMYKGVTKKIDELVELVGLK 123

Db 67 FGKDLKQHRLDILKNIGALVESPSYVPHLSGSDNLETVRKIVK-VPKSRIAEVLVRLT 125

QY 124 NRINDKVTYSIGMQRGLAQSLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREGK 183

Db 126 KVADRKVOEYSLGMQRGLAQSLHDPKLLILDEPTNGLDPAGIREIRDYLRKLTREGK 185

QY 184 MAVIVSSHLSSMELMCDRIATIQNGKLRDIOHVHGPARDKKYVYIQADDTQALTREA 243

Db 186 ITVLSHLLSEVEQVAGVGIAGKLIQFQDSIELRKKANKRIFLSTSHPEV----AA 241

QY 244 AF---RKVKVDEAEGGIELSIQKD-EVPDLIKHLTDGVRVLYEVKAVNKSLEDRFLEIT 298

Db 242 TTILQERGINVDQARGLVNDRSDEIAQLVKAFAVEKIDIVYRISDETSSLEEIFLQLT 300

RESULT 9

ADN27185

ID ADN27185 standard; protein; 299 AA.

XX AC ADN27185;

XX 02-DEC-2004 (first entry)

XX Bacterial polypeptide #9838.

XX Recombinant DNA construct; transformed plant; improved plant property;

KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;

KW pathogen tolerance; pest tolerance; plant disease resistance;

KW cell cycle pathway modification; plant growth regulator;

KW homologous recombination; seed oil yield; protein yield; carbohydrate;

KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

XX bacterial polypeptide.

OS Bacteria.

XX US2003233675-A1.

PN 18-DEC-2003.

PD 20-FEB-2003; 2003US-00369493.

PF 21-FEB-2002; 2002US-0360039P.

PR (CAOY/) CAO Y.

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

PI WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide

PT for expression of a polynucleotide encoding a polypeptide from a

PT microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 9838; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a

CC promoter functional in a plant cell, where the promoter is positioned to

CC provide for expression of a polynucleotide encoding a polypeptide from a

CC microbial source, useful for producing plants with improved properties.









CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition. Improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
XX  
SQ Sequence 308 AA;

Query Match 32.0%; Score 493; DB 8; Length 308;  
Best Local Similarity 36.4%; Pred. No. 1e-35;  
Matches 118; Conservative 67; Mismatches 91; Indels 48; Gaps 7;  
QY 5 LELKNVSKTIRGKKIIEGLSPDVRAGIFGLPGNGAGKTTIRMIIVGHSITAGETAVC 64  
DB 4 IEVKLTYSYKFKAINLSFVDEGVFGFLPGNGAGKTTIILSLGIIIPDSGDVRL 63  
QY 65 GVSVKENFEKAARHIGAIVENPELYKLTGYQLQOYA---RMTKVTGKKIDIBEVLVG 121  
DB 64 GYDIFKEPLKAKERGLPENATYIELTAWNLDPFASFVMSKQEKKEIEBLLKVG 123  
QY 122 LKNRINDKVTYSLGMQRGLAQSLHDPKLLIDEPNGLDPAGIRIRDYLRKLTRE 181  
DB 124 LWDVRYKAKTFSGMQRQLLAQALINDPELLIDEPNGLDPAGIRIRDYLRKLTRE 182  
QY 182 KGAVIVSSHLSEMELMCDRIATIQNGKLRDIOHVGPAREDEKRYVIQADDTQALRE 241  
DB 183 QGKTVFSSHLSEVELADKVGIIIVKGLRTV---GTLEEIKQY-----ME 227  
QY 242 AAARFKVKVDEAEGGIELSIQKDEVPDLIK-----HLTDSGV 278  
DB 228 LEGY-EIKETKQPLP-----EIPDIIEKTKTENKAIIFAKSDIREISELAKKGI 281  
QY 279 RLYEVKAVNKSLEDRFLEITADKE 302  
DB 282 TIISLEIEEPSLEVDVFLKTYRRE 305

RESULT 13  
ADN18683  
ID ADN18683 standard; protein; 318 AA.

AC ADN18683;  
XX  
XX  
DT 02-DEC-2004 (first entry)  
DE Bacterial polypeptide #1336.  
XX  
KW Recombinant DNA construct; transformed plant; improved plant property;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
KW pathogen tolerance; pest tolerance; plant disease resistance;  
KW cell cycle pathway modification; plant growth regulator;  
KW homologous recombination; seed oil yield; protein yield; carbohydrate;  
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
KW bacterial polypeptide.

OS Bacteria.

XX US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX

PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
XX  
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX WPI; 2004-061375/06.  
XX  
XX New recombinant DNA construct comprising a promoter positioned to provide  
XX for expression of a polynucleotide encoding a polypeptide from a  
XX microbial source, useful for producing plants with improved properties.  
XX  
XX Claim 1; SEQ ID NO 1336; 122pp; English.

CC The invention relates to a recombinant DNA construct comprising a  
CC promoter functional in a plant cell, where the promoter is positioned to  
CC provide for expression of a polynucleotide encoding a polypeptide from a  
CC microbial source. The invention also relates to a transformed plant  
CC comprising the recombinant DNA construct and a method of producing a  
CC transformed plant having an improved property. The plant is a crop plant  
CC such as maize or soybean. The method of producing a transformed plant  
CC having an improved property comprises transforming a plant with the  
CC recombinant DNA construct and growing the transformed plant, where the  
CC polynucleotide or polypeptide is useful for improving plant properties.  
CC The recombinant DNA construct is useful for producing plants with  
CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
CC increased resistance to plant disease, better growth rate by modification  
CC of the cell cycle pathway with plant growth regulators, increased rate of  
CC homologous recombination, modified seed oil or protein yield and/or  
CC content, improved yield by modification of carbohydrate, nitrogen or  
CC phosphorus use and/or uptake, by modification of photosynthesis or by  
CC providing improved plant growth and development under at least one stress  
CC condition. Improved lignin production or improved galactomannan  
CC production. This sequence represents a bacterial polypeptide used in the  
CC scope of the invention. Note: The sequence data for this patent did not  
CC form part of the printed specification but was obtained in electronic  
CC format from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
XX SQ Sequence 318 AA;

Query Match 31.9%; Score 491.5; DB 8; Length 318;  
Best Local Similarity 35.2%; Pred. No. 1.5e-35;  
Matches 112; Conservative 78; Mismatches 97; Indels 31; Gaps 7;

QY 4 LLELKNVSKTIRGKKI-----IEGLSPDVRAGIFGLPGNGAGKTTIRMIIV 51  
DB 3 VIEVRNLK-LYPKKIPLPKRVKVEPEALAGITFRVKKGELFGLPGNGAGKTTIKILT 61  
QY 52 GHMSITAGETAVCGSVKVENFEKAARHIGAIVENPE-LYKLTGYQLQOYAR---MTKG 107  
DB 62 TLLEPSGSEAKVLGLDWWKADAREIKRINLVAEGERTLYWRLTAYENLRVPASTYIYIPRR 121  
QY 108 VTKKKYDEIVELVGLKNRINDKVTYSLGMQRGLAQSLHDPKLLIDEPNGLDPAG 167  
DB 122 EAEKRIEELKMWGLMDRRNDLVNYSRGMKQRIATIAKALINDPEVLDFLEPTGLDVOQS 181  
QY 168 IREIRDYLRKLTRKGMNAVIVSSHLSEMELMCDRIATIQNGKLRDIOHVGPAREDEK 227  
DB 182 AVFVRELVRVLDVEGKTVLLTTHYMNABELCDRIATIDHGKIATLTPESGLK- 236  
QY 228 YIIQADDTQALTR-----EAAAFKRVKVDABEGGIEL--SIQKDEVPDLIKHLTDSGVRL 280  
DB 237 --MVRNDTIVEVRVRYNYPGVNPFGLVKVDDRRNGVILRGSLEBEEIPKLVFKVSKNAK 294  
QY 281 YEYKAVNKSLEDRPLEIT 298  
DB 295 LSVEVKEPTLEDVFIKLT 312

RESULT 14





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GenCore version 5.1.9  
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OM protein - protein search, using sw model  
Run on: July 13, 2006, 13:44:12 ; Search time 40 Seconds  
(without alignments)  
738.464 Million cell updates/sec

Title: US-10-510-941-2  
Perfect score: 1542  
Sequence: 1 LETLLEKNVSKTIRGKKII.....KSLDRFLEITADKBEAQHV 307  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1027	66.6	305	2 D69822	ABC transporter (A
2	734	47.6	301	2 AD1169	ABC transporter (A
3	730	47.3	301	2 AF1526	Similar to ABC tra
4	680	44.1	312	2 G96916	ABC transporter, A
5	671.5	43.5	308	2 E69771	ABC transporter, A
6	667	43.3	318	2 H96917	ABC transporter, A
7	641	41.6	306	2 AD1642	ABC transporter (A
8	639	41.4	306	2 AD1279	ABC transporter (A
9	638	41.4	300	2 D97272	protein from GDSL
10	535.5	34.7	306	2 E83705	ABC transporter (A
11	528.5	34.3	242	2 B96935	ABC transporter, A
12	523	33.9	306	2 D97151	ABC transporter MD
13	515	33.4	306	2 S77827	bacitracin transpo
14	512	33.2	306	2 T31682	bcrA protein - Bac
15	504.5	32.7	299	2 T09008	probable ATP-bind
16	493	32.0	308	2 H71008	probable ATP-bind
17	491.5	31.9	318	2 C71197	probable ATP-bind
18	486	31.5	307	2 H83705	ABC transporter (A
19	484	31.4	301	2 JCS348	cdd4 protein - Clo
20	475	30.8	314	2 D97318	ABC-type MDR trans
21	473	30.7	305	2 E75122	hypothetical prote
22	471	30.5	314	2 B83752	bacitracin ABC tra
23	464	30.1	311	2 G69803	ABC transporter (A
24	463.5	30.1	294	2 G69391	ABC transporter, A
25	463.5	30.1	312	2 G97260	ABC-type MDR trans
26	461.5	29.9	313	2 G97006	ABC-type multidrug
27	451.5	29.3	318	2 H75157	daunorubicin resis
28	450	29.2	307	2 B97006	ABC-type multidrug
29	444.5	28.8	312	2 T29454	ABC transport prot

30	442.5	28.7	901	2 F83781	transposase (08) /
31	431.5	28.0	258	2 F96932	ABC transporter AT
32	431.5	28.0	339	2 AE2102	ABC transporter AT
33	430.5	27.9	311	2 F87655	ABC transporter, A
34	428	27.8	331	2 AE2008	spaf protein - Bac
35	425	27.6	456	1 I40516	ABC transporter (A
36	424.5	27.5	312	2 C69012	ABC transporter (A
37	424	27.5	298	2 T43103	ABC transport prot
38	422.5	27.4	310	2 E96920	ABC transporter (A
39	421.5	27.3	298	2 T44443	gliding motility p
40	421.5	27.3	310	2 B83912	ABC transporter (A
41	421	27.3	327	2 D72257	hypothetical prote
42	420.5	27.3	282	2 E84136	ABC transporter (A
43	420.5	27.3	317	2 T36316	probable ABC-type
44	420	27.2	301	2 B83686	ABC transporter (A
45	420	27.2	312	2 G71131	probable ATP-bind

ALIGNMENTS

RESULT 1  
D69822  
ABC transporter (ATP-binding protein) homolog yhcH - Bacillus subtilis  
C;Species: Bacillus subtilis  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 05-Oct-2004  
C;Accession: D69822  
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte  
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch  
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrati, E  
Nature 390, 249-256, 1997  
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holstappel, S.; Hosono, S.; Hullo, M.F  
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinol  
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue  
Y, M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon  
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowaka, A.; Sero  
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiyama  
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,  
A;Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.  
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis  
A;Reference number: A69580; MUID:98044033; PMID:9384377  
A;Accession: D69822  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-305 <KUN>  
A;Cross-references: UNIPROT:P54592; UNIPARC:UPI0000060122; GB:Z99108; GB:AL009126; NID  
A;Experimental source: strain 168  
C;Genetics:  
A;Gene: yhcH  
C;Keywords: ATP; nucleotide binding; P-loop  
F;20-209/Domain: ATP-binding cassette homology <ABC>  
F;37-44/Region: nucleotide-binding motif A (P-loop)

Query Match	66.6%	Score	1027	DB	2	Length	305
Best Local Similarity	65.1%	Pred. No.	1.3e-57				
Matches	200	Conservative	47	Mismatches	56	Indels	4
Gaps	2						
QY	1	LETLLEKNVSKTIRGKKII	EGLSFDVRAGEIFGFLGPNAGAGKTTTIRMIVGHMSITAGE	60			
Db	1	MKTVLKKNVKNIRGRTI	DDLSFTIREGEVFGFLGPNAGAGKTTTIRMVGLMKLSKGD	60			
QY	61	IACVGVSVKENFKAARHGA	IVENPELYKFLTGYNLQYARMTKGVTKKKIDIEIVELY	120			
Db	61	VLICGQSITKEVAKAIKHA	IVENPELYKFLSGYKNLQGFARMKVGVTKKIDIEIVELY	120			
QY	121	GLKNRINDKVTYSLGWRQEL	GLAQSLHDPKLLIILDEPTNGLDPAIRIRYLKLT	180			
Db	121	GLTDRIHDKVTYSLGWRQEL	GLAQSLHDPKLLIILDEPTNGLDPAIRIRYHKL	180			
QY	181	EKGMAIVSVSHLLSELMEL	CMCDRIATIQNGKLRDIQHVHGPARDEKKRYIQADDTQ	240			





RESULTS 6  
H96917  
ABC transporter, ATP-binding protein CAC0147 [imported] - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 05-Oct-2004  
C:Accession: H96917  
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.;  
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001

A;Title: genome sequence and comparative analysis of the solvent-producing bacterium  
A;Reference number: A96900; MUID:21359325; PMID:21359325  
A;Accession: H96917  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-318 <KUR>  
A;Cross-references: UNIPROT:Q97WPS; UNIPARC:UPI000000C9D8B; GB:AE001437; PIDN:AAK7813  
A;Experimental source: Clostridium acetobutylicum ATCC824  
C;Genetics:  
A;Gene: CAC0147

Qy	121	GLKORINDKVKYTSGLNQRQGLAQSLHDPKLLILDEPTNGLDPPAGIREIRDYLRKLT	180
Db	121	GLSRLDERKVKYTSGLNQRQGLAEALISKPCLLILDEPTNGLDPTGIISEPNLLKKQAK	180
Qy	181	EKGMAVIVSHLLSEMELMCDRIATIQNGKLRDIQHVHGPARDKKRYITQADDTQALTR	240
Db	181	ENKWAIFVSSHIIISEIEQLCDRVAFIDGGIIKSFETLKGTKNKHKTSEF---ENVVIMTK	237
Qy	241	E-----AAAFPRVK-----VDAEG--GIELSIQKDEVPDLIKHLTDSGVRLYEYKAVN	287
Db	238	EKDCKTEALKEISFIIDFKLADSSNGIYTFEAKAKLDSVDITSSLAEKKIRIEQIVKQR	297
Qy	288	KSLEDRFLEI	297
Db	298	ONLEDREVIEL	307

Qy	288	KSLEDRFLEI	297
	:		:
Db	298	ONLEDRYTEL	307

RESULT 7  
AD1642  
ABC transporter (ATP-binding protein) homolog lin1677 [imported] - *Listeria innocua*  
C/Species: *Listeria innocua*  
C/Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 31-Dec-2004  
C/Accession: AD1642  
R/Glaeser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloesch,  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Fsihi  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkak, G.; Madueno, E.; Maitournam, A.;  
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlh  
A/Title: Comparative genomics of *Listeria* species.  
A/Reference number: AB1077; MUID:21537279; PMID:11679669  
A/Accession: AD1642  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-306 <GLA>  
A/cross-references: UNIPROT:Q92B73; UNIPARC:UP100000CC61A; GB:AL592022; PIDN:CAC96908E08  
A/experimental source: strain Clip11262  
C/Genetics:  
A/Gene: lin1677

Query Match 41.6% Score 641 DB 2 Length 306

Best Local Similarity 45.0%; Pred. No. 2.5e-33;  
Matches 134; Conservative 59; Mismatches 103; Indels 2; Gaps 2;  
QY 2 ETLLKLVNKTIRGKKIIIEGLSFDVRAGEIFGFLGPNAGAGKTTIRIMVGHMSITAGEI 61  
DB 3 ETVLKLEHVTKIGQKNIIVHDISFDTHKGEVFLGPNAGAGKTTIRSVGLIRRSEGT 62  
QY 62 AVCGSVKVFENFEKAARHIGAIVENPELYKFLTGYNLQOYARMT-KGVTKKKIDEIVELV 120  
DB 63 YINGKNVIDFKAALISEVGAIIENPEFYMGWGANLKQFARMSQKNITDHIRIIVELV 122  
QY 121 GLKNRINDKVTYSLGMRQRLGLAQLLHDPKLLILDEPTNGLDPAQIRIRDYRLKLT 180  
DB 123 KLSDAINQKVITYSLGMRQRLGLAQLLHDPKLLILDEPTNGLDPAQIRIRDYRLKLT 181  
QY 181 EKGMAVIVSHLLSEMLMCDRIAIIQNGKLRDIQHVHGPARDKRYVYIQADDTQALTR 240  
DB 182 TNGTSVLISHLSEIQQITDRFAIINKGVLTHTEKMSDVLENHVAVYQLKVTDSVAAKT 241  
QY 241 EAAAFKVKVDEAEGGIELSQKDEVPDLIKHLTDSGVRLYEKAVNKSLDRFLEIT 298  
DB 242 VLATLPVKLVAKENSKFIEVAHEDVHLIARAIQAIQANIDLEMMVPLQASLEERFLEIT 299  
RESULT 8  
AD1279  
ABC transporter (ATP-binding protein) homolog lmo1636 [imported] - Listeria monocytogenes  
C:Species: Listeria monocytogenes  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 31-Dec-2004  
C:Accession: AD1279  
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, R.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitourman, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative Genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AD1279  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-306 <GLA>  
A:Cross-references: UNIPROT:Q8Y6P8; UNIPARC:UPI0000055004; GB:NC\_003210; PIDN:CAC99714.1  
A:Experimental source: strain EGD-e  
C:Genetics:  
A:Gene: lmo1636

Query Match 41.4%; Score 639; DB 2; Length 306;  
Best Local Similarity 45.3%; Pred. No. 3.4e-33;  
Matches 135; Conservative 57; Mismatches 104; Indels 2; Gaps 2;  
QY 2 ETLLKLVNKTIRGKKIIIEGLSFDVRAGEIFGFLGPNAGAGKTTIRIMVGHMSITAGEI 61  
DB 3 ETVLKLEHVTKIGQKNIIVHDISFDTHKGEVFLGPNAGAGKTTIRSVGLIRRSEGT 62  
QY 62 AVCGSVKVFENFEKAARHIGAIVENPELYKFLTGYNLQOYARMT-KGVTKKKIDEIVELV 120  
DB 63 YINGKNVIDFKAALISEVGAIIENPEFYMGWGANLKQFARMSQKNITDHIRIIVELV 122  
QY 121 GLKNRINDKVTYSLGMRQRLGLAQLLHDPKLLILDEPTNGLDPAQIRIRDYRLKLT 180  
DB 123 KLSDAINQKVITYSLGMRQRLGLAQLLHDPKLLILDEPTNGLDPAQIRIRDYRLKLT 181  
QY 181 EKGMAVIVSHLLSEMLMCDRIAIIQNGKLRDIQHVHGPARDKRYVYIQADDTQALTR 240  
DB 182 TNGTSVLISHLSEIQQITDRFAIINKGVLTHTEKMSDVLENHVAVYQLKVTDSVAAKT 241  
QY 241 EAAAFKVKVDEAEGGIELSQKDEVPDLIKHLTDSGVRLYEKAVNKSLDRFLEIT 298  
DB 242 VLATLPVKLVAKENSKFIEVAHEDVHLIARAIQAIQANIDLEMMVPLQASLEERFLEIT 299  
RESULT 9

D97272  
protein from GDSL (phospholipase B) family of lipolytic enzymes [imported] - Clostridium  
C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 05-Oct-2004  
C:Accession: D97272  
R:Nolling, J.; Brencon, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: D97272  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-300 <KUR>  
A:Cross-references: UNIPROT:Q97ET0; UNIPARC:UPI0000007564; GB:AE001437; PIDN:AAK80967.1  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC3026

Query Match 41.4%; Score 638; DB 2; Length 300;  
Best Local Similarity 40.7%; Pred. No. 3.8e-33;  
Matches 122; Conservative 85; Mismatches 87; Indels 6; Gaps 4;  
QY 4 LLELKNVSKTIRGKKIIIEGLSFDVRAGEIFGFLGPNAGAGKTTIRIMVGHMSITAGEI 63  
DB 5 ILLVEDVHKVIRGEIIRKINFSIDEGEVLGFLGPNAGAGKTTIRIMVGHMSITAGEI 64  
QY 64 CGSVKVFENFEKAARHIGAIVENPELYKFLTGYNLQOYARMT-KGVTKKKIDEIVELV 123  
DB 65 CGYSLHNVVKAVESGVCIVEGPDLYEYMGSDNLEMLAAMDKNVTNEDIEYAVNLVME 124  
QY 124 NRINDKVTYSLGMRQRLGLAQLLHDPKLLILDEPTNGLDPAQIRIRDYRLKLTREK 183  
DB 125 KSIKDKISTYSLGMRQRLGLAQLLHDPKLLILDEPTNGLDPAQIRIRDYRLKLTREK 184  
QY 184 MAVIVSHLLSEMLMCDRIAIIQNGKLRDIQHVHGPARDKRYVYIQADDTQALTR 243  
DB 185 ISVLSSHLIARIEIETCDKVSIIKQGEI--LKNASVAELLKTKYEVFWELNDNEK-GR 241  
QY 244 AFRKVKVDEAEGG--IELSIQKDEVPDLIKHLTDSGVRLYEKAVNKSLDRFLEIT 301  
DB 242 K-NSWRIDSRINGSKLEASVDEEKLISINDSFLSNGIKIKFASSKQRLNEDLFNIT 300

RESULT 10  
E83705  
ABC transporter (ATP-binding protein) BH0445 [imported] - Bacillus halodurans (strain C  
C:Species: Bacillus halodurans  
C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 05-Oct-2004  
C:Accession: E83705  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir  
Nucleic Acids Res. 28, 4317-4331, 2000  
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A:Reference number: A83650; MUID:20512582; PMID:11058132  
A:Accession: E83705  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-306 <STO>  
A:Cross-references: UNIPROT:Q9KFN4; UNIPARC:UPI000000C38A0; GB:AF001508; GB:BA000004; N  
A:Experimental source: strain C-125  
C:Genetics:  
A:Gene: BH0445

Query Match 34.7%; Score 535.5; DB 2; Length 306;  
Best Local Similarity 38.5%; Pred. No. 1.1e-26;  
Matches 115; Conservative 69; Mismatches 106; Indels 9; Gaps 4;  
QY 4 LLELKNVSKTIRGKKIIIEGLSFDVRAGEIFGFLGPNAGAGKTTIRIMVGHMSITAGEI 63  
DB 7 LIETNNLTMTYKHVHVAVDRLNKLKVEGEIYGFGLGPNAGAGKTTIRIMVGHMSITAGEI 66  
QY 64 CGSVKVFENFEKAARHIGAIVENPELYKFLTGYNLQOYARMT-KGVTKKKIDEIVELV 123

Db 67 FGDKLQKRLDILKNIGALVESPSYPHLSGEDNLETVRKIVK-VPKSRIAEVLVRLT 125  
Qy 124 NRINDKVTYSLGMRQRLGLAQLSDPKLILDEPTNGLDPAQIRREIRDLRLTREKG 183  
Db 126 KVADKKVQVSLGMRQRLGLAQLSDPKLILDEPTNGLDPAQIRREIRDLRLTREKG 185  
Qy 184 MAVIVSHLLSEMLMCDRIAIQNGKLRDIOHVHGPARDKKRYIIQADDTQALTRAA 243  
Db 186 ITVLSSHLSEVEQASQVGIAGKLIQFSDIEELRKANRKFILSTSHPEV-AAA 241  
Qy 244 AF---RKVKDEAGGIELSTQKD-EVPDLIKHITDSGRLYEYKAVNKSLDEFLRIT 298  
Db 242 TIQERGINVDQARGLVMDNRSDIEEAQLVKAFVEKDIDVIRISDETSSLEELQIT 300  
RESULT 11  
B96935  
ABC transporter, ATP-binding protein CAC0288 [imported] - Clostridium acetobutylicum  
C;Species: Clostridium acetobutylicum  
C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 31-Dec-2004  
C;Accession: B96935  
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld  
A;Reference number: A96900; MUID:21359325; PMID:21359325  
A;Accession: B96935  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-242 <KUR>  
A;Cross-references: UNIPROT:Q97WB0; UNIPARC:UPI00000C9DFE; GB:AE001437; PIDN:AAK78269.1;  
A;Experimental source: Clostridium acetobutylicum ATCC824  
C;Genetics:  
A;Gene: CAC0288

Query Match 34.3%; Score 528.5; DB 2; Length 242;  
Best Local Similarity 48.6%; Pred. No. 2.3e-26;  
Matches 101; Conservative 49; Mismatches 57; Indels 1; Gaps 1;  
Qy 4 LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAGE 63  
Db 5 VVEINLSKTYRGFNNAVNNINLIREGRIYVGLGPNAGKSTTIRMILGLIKNSGSIKI 64  
Qy 64 CGVSVKENFEKAARHIGAIVENPELYKFLATGYQNLQOYARMTKGVTKKIDIEIVELVGLK 123  
Db 65 FGKLNKENRAEILKNGVALVESPSYGHNLAYENLKIWSYI-XGVDKNAIDEVLKGLVNL 123  
Qy 124 NRINDKVTYSLGMRQRLGLAQLSDPKLILDEPTNGLDPAQIRREIRDLRLTREKG 183  
Db 124 EHRKKVSKFSLGMRQRLGLAQLSDPKLILDEPTNGLDPAQIRREIRDLRLTREKG 183  
Qy 184 MAVIVSHLLSEMLMCDRIAIQNGKLRDIOHVHGPARDKKRYIIQADDTQALTRAA 211  
Db 184 KTIISHSILSEMLMCDRIAIQNGKLRDIOHVHGPARDKKRYIIQADDTQALTRAA 211

RESULT 12  
D97151  
ABC transporter MDR-type, ATPase component CAC2040 [imported] - Clostridium acetobutylicum  
C;Species: Clostridium acetobutylicum  
C;Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 05-Oct-2004  
C;Accession: D97151  
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld  
A;Reference number: A96900; MUID:21359325; PMID:21359325  
A;Accession: D97151  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-306 <KUR>  
A;Cross-references: UNIPROT:Q97HH1; UNIPARC:UPI00000CA3C9; GB:AE001437; PIDN:AAK79999.1;  
A;Experimental source: Clostridium acetobutylicum ATCC824

C;Genetics:  
A;Gene: CAC2040  
Query Match 33.9%; Score 523; DB 2; Length 306;  
Best Local Similarity 39.5%; Pred. No. 6.6e-26;  
Matches 121; Conservative 65; Mismatches 106; Indels 14; Gaps 6;  
Qy 1 LETLLEKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAGE 60  
Db 1 MKYLVRFTNLTKYKNTSVVENLNIEQOYIGFLGKNAGKTTTIRMILGLMKISITGE 60  
Qy 61 IAVCGSVKENFEKAARHIGAIVENPELYKFLATGYQNLQOYARMTKGVTKKIDIEIVELV 120  
Db 61 VELFG--EKNPRTSIYKKGISIIIEYPGFYNLTAEENLDIHRMMKIENQKXINETLTMV 118  
Qy 121 GL-KNRI-NDKVTYSLGMRQRLGLAQLSDPKLILDEPTNGLDPAQIRREIRDLRLTRE 178  
Db 119 GLDSNISKVKKNFSLGMRQRLGLAQLSDPKLILDEPTNGLDPAQIRREIRDLRLTRE 178  
Qy 179 TREKGMVIVSSHLSEMLMCDRIAIQNGKLRDIOHVHGPARDKKRYIIQADDTQAL 238  
Db 179 CKDGRITILVSSHLSEMLMCDRIAIQNGKLRDIOHVHGPARDKKRYIIQADDTQAL 234  
Qy 239 TREAAAFRK---VKVDEAEG--GIELSIOKDEVPDLIKHITDSGRLYEYKAVNKSLDE 292  
Db 235 VKEACSLIKNNLAKDYIEIGKDAIKYVEKINESSTIAKLIKNDIELYEMSFSDKNLE 294  
Qy 293 RFLRIT 298  
Db 295 YFVKVT 300  
RESULT 13  
S77627  
bacitracin transport protein bcrA - Bacillus licheniformis  
C;Species: Bacillus licheniformis  
C;Date: 24-Oct-1998 #sequence\_revision 24-Oct-1998 #text\_change 05-Oct-2004  
C;Accession: S77627  
R;Podlessek, Z.; Comino, A.; Herzog-Velikonja, B.; Zgur-Bertok, D.; Komel, R.; Grabnar, M.; Mol. Microbiol. 16, 969-976, 1995  
A;Title: Bacillus licheniformis bacitracin-resistance ABC transporter: relationship to  
A;Reference number: S77627; MUID:96059642; PMID:7476193  
A;Accession: S77627  
A;Molecule type: DNA  
A;Residues: 1-306 <POD>  
A;Cross-references: UNIPROT:P42332; UNIPARC:UPI0000126845; EMBL:IL20573; NID:9466477; PI  
A;Experimental source: strain ATCC 9945A  
C;Genetics:  
A;Gene: bcrA  
A;Start codon: TTG  
C;Keywords: antibiotic resistance; ATP binding; nucleotide binding; P-loop  
F;20-209/Domain: ATP-binding cassette homology <ABC>  
F;37-44/Region: nucleotide-binding motif A (P-loop)  
Query Match 33.4%; Score 515; DB 2; Length 306;  
Best Local Similarity 36.6%; Pred. No. 2.1e-25;  
Matches 113; Conservative 76; Mismatches 98; Indels 22; Gaps 5;  
Qy 1 LETLLEKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAGE 60  
Db 1 MSTIITKTDLTLMYGSQKSVHDHINVKQDIYVGLGRNAGKTTTIRMILGLIKPTSGG 60  
Qy 61 IAVCGSVKENFEKAARHIGAIVENPELYKFLATGYQNLQOYARMTKGVTKKIDIEIVEL 119  
Db 61 IEIFGFENFPKKEILLRIGSIIEVPGFYANLTARENLLINAKII-GIHKNAIDEVLEI 119  
Qy 120 VGLKNRINDKVTYSLGMRQRLGLAQLSDPKLILDEPTNGLDPAQIRREIRDLRLTRE 179  
Db 120 VGLQHEKTKLVGKFSGLGMRQRLGLAQLSDPKLILDEPTNGLDPAQIRREIRDLRLTRE 179  
Qy 180 REKGMVIVSSHLSEMLMCDRIAIQNGKLRDIOHVHGPARDKKRYIIQADDTQAL 238  
Db 180 KERNITIFISSHLSEMLMCDRIAIQNGKLRDIOHVHGPARDKKRYIIQADDTQAL 239

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QY 239 TREAAAFRKVKVDEAEGGIELSIQKDEVPDLIKHL-----TDSGVRLYEVKAVNK 288
Db 240 -----VLMQHFHDHDEYHQDGIIRVYSHLQOQKLNKLFVENGIDVLKITMSD 290
QY 289 SLEDRFLEI 297
Db 291 SLEDYFVKL 299

RESULT 14
T31682
bczA protein - Bacillus licheniformis
C;Species: Bacillus licheniformis
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 05-Oct-2004
C;Accession: T31682
R;Könz, D.; Klens, A.; Schorgendorfer, K.; Marahiel, M.A.
Chem. Biol. 4, 937-937, 1997
A;Title: The bacitracin biosynthesis operon of Bacillus licheniformis ATCC 10716: molecu
A;Reference number: 221058; MUID:98089193; PMID:9427658
A;Accession: T31682
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-306 <KON>
A;Cross-references: UNIPROT:Q9SSV9; UNIPARC:UPI00000AF215; EMBL:AF007865; NID:94464275;
C;Genetics:
A;Gene: bczA

Query Match 33.2%; Score 512; DB 2; Length 306;
Best Local Similarity 36.2%; Pred. No. 3.3e-25;
Matches 112; Conservative 76; Mismatches 99; Indels 22; Gaps 5;

QY 1 LETLLELKNVSKTIRGKKIIEGLSFQVRAGEIFGFLGPNAGAGTKTTIRMIVGHMSITAGE 60
Db 1 MSTIIKTTDLTKWYGSQKSDHNLNINVKQGDIVGFLGRNGAGTKTTIRMLLGLIKETSGQ 60
QY 61 IAVCGSVSKENFEKAARHIGAIIVENPELYKFLTGYNLQOYARMTKGVTKKK-IDBIVEL 119
Db 61 IEIFGENFFKNKEILLRIGSIVEVPGFYANLTARENLLINAKII-GIHKKNALDEVLEI 119
QY 120 VGLKNRINDKVTYSLGMORQLGLAOSLLHDPKLLILDEPTNGLDLPAGIREIRDYLRKL 179
Db 120 VGLQHETKVLGVKFSLGMQKQLGARALLHYPSELSILDEPTNGLDPIGIKEMERLIHSLA 179
QY 180 REKGMVIVSSHLLSEMELMCDRIATIIQNGK-LRDIQHVHGPARDEKRYIIQADDTQAL 238
Db 180 KERNITFISSHLSEIEQVHDVHGIIHEGKLLBEPFDHLKRNKYLEFQLSDQNKAV 239
QY 239 TREAAAFRKVKVDEAEGGIELSIQKDEVPDLIKHL-----TDSGVRLYEVKAVNK 288
Db 240 -----VLMQHSDDHDEYHQDGIIRVYSHLQOQKLNKLFVENGIDVLKITMSD 290
QY 289 SLEDRFLEI 297
Db 291 SLEDYFVKL 299

RESULT 15
T09008
cdd4-like protein ScnF - Streptococcus pyogenes
C;Species: Streptococcus pyogenes
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 05-Oct-2004
C;Accession: T09008
R;Hynes, W.L.; Ferretti, J.J.; Tagg, J.R.
Appl. Environ. Microbiol. 59, 1963-1971, 1993
A;Title: Cloning of the gene encoding streptococcin A-FF22, a novel lantibiotic produced
A;Reference number: A58598; MUID:93319301; PMID:8328813
A;Accession: T09008
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-299 <HYN>
A;Cross-references: UNIPROT:O31054; UNIPARC:UPI00000B5C5D; EMBL:AF026542; NID:92502065;
A;Experimental source: strain FF22
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C;Genetics:
A;Gene: scnF
C;Keywords: antibiotic biosynthesis
P:20-209/Domain: ATP-binding cassette homology <ABC>

Query Match 32.7%; Score 504.5; DB 2; Length 299;
Best Local Similarity 39.4%; Pred. No. 9.4e-25;
Matches 121; Conservative 59; Mismatches 102; Indels 25; Gaps 6;

QY 1 LETLLELKNVSKTIRGKKIIEGLSFQVRAGEIFGFLGPNAGAGTKTTIRMIVGHMSITAGE 60
Db 1 MKNALIELKLSKVYQDITTVDEKLTIVREGEIYGLGPNAGAGTKTTMKWILSLVSPTLGE 60
QY 61 IAVCGSVSKENFEKAARHIGAIIVENPELYKFLTGYNLQOYARMTKGVTKKKIDIEVELV 120
Db 61 ILINGEDIKGN-HAYLRVIGSMIEPSYVPLNTGYENLLVFQKVV-GPDESNIWPTLALV 118
QY 121 GLKNRINDK--VKTYSLGNRQRLGLAOSLLHDPKLLILDEPTNGLDLPAGIREIRDYLRKL 178
Db 119 GLAENNRKLVKAYSGLGMQKQLGARALLHYPSELSILDEPTNGLDPIGIRELIVKL 178
QY 179 TREKGMVIVSSHLLSEMELMCDRIATIIQNGK---RDIQHVHGPARDEKRYIIQADDT 235
Db 179 AKKGLTVFISSQIILSEIEHIADRVGIINHGRVYVEGEIEAKSNWTWIEIGDFSQNNIV 238
QY 236 QALTR-----EAAAFRKVKVDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVN 287
Db 239 QSLINVQVEVLGASASHVKFK-----NIDNDKLADVGTVLIENDYRIFRVRES 288
QY 288 KSLDRPF 294
Db 289 ENLEDIF 295

Search completed: July 13, 2006, 13:49:44
Job time : 41 secs
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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 13, 2006, 13:40:51 ; Search time 298 seconds  
(without alignments)  
952.952 Million cell updates/sec

Title: US-10-510-941-2

Perfect score: 1542

Sequence: 1 LETLLEKNVSKTIRGKKII.....KSLEDRFLEITADKBAQHV 307

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot\_7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1540	99.9	307	2	Q65M37_BACLD
2	1027	66.6	305	1	YHCH_BACSU
3	806	52.3	307	2	Q8EQ15_OCEIH
4	789	51.2	300	2	Q61117_BACAN
5	789	51.2	300	2	Q6HLJ0_BACHK
6	785	50.9	300	2	Q4MSI3_BACCE
7	785	50.9	300	2	Q73BE3_BACC1
8	784	50.8	300	2	Q3EML1_BACPI
9	783	50.8	300	2	Q63E15_BACZ
10	781	50.6	300	2	Q81G51_BACCR
11	754.5	48.9	305	2	Q6HAN5_BACHK
12	748.5	48.5	305	2	Q81JQ2_BACAN
13	744.5	48.3	305	2	Q3EW61_BACPI
14	743.5	48.2	305	2	Q72X49_BACC1
15	739.5	48.0	305	2	Q4MLR2_BACCE
16	739.5	48.0	305	2	Q814M7_BACCR
17	738	47.9	306	2	Q81AB3_BACIL
18	735.5	47.7	305	2	Q63OK0_BACZ
19	734	47.6	301	2	Q8Y8V6_LISMO
20	733	47.5	331	2	Q6HFD4_BACHK
21	733	47.5	331	2	Q73F8_BACC1
22	731	47.4	320	2	Q4MNN2_BACCE
23	730	47.3	301	2	Q92DR3_LISIN
24	728	47.2	301	2	Q4EUC2_LISMO
25	728	47.2	331	2	Q637G1_BACZ
26	727	47.1	301	2	Q4ELV1_LISMO
27	727	47.1	301	2	Q72F3_LISMF
28	712	46.2	308	2	Q5KZF8_GEOKA
29	709	46.0	268	2	Q81YB0_BACAN
30	680	44.1	312	2	Q97MQ4_CLOAB
31	672	43.6	306	2	Q41AX1_9BACI

32	671.5	43.5	308	2	P96605_BACSU
33	670	43.5	304	2	Q2WL76_CLOBE
34	667	43.3	318	2	Q97MP5_CLOAB
35	666.5	43.2	307	2	Q5W112_BACSK
36	663	43.0	308	2	Q65N71_BACLD
37	660.5	42.8	319	2	Q81CN4_BACCR
38	658.5	42.7	303	2	Q895C2_CLOTE
39	641	41.6	306	2	Q92B73_LISIN
40	639	41.4	306	2	Q4EMV3_LISMO
41	639	41.4	306	2	Q8Y6P8_LISMO
42	638	41.4	300	2	Q65DD4_BACLD
43	638	41.4	300	2	Q97ET0_CLOAB
44	638	41.4	306	2	Q4EEG7_LISMO
45	638	41.4	306	2	Q71232_LISMF

#### ALIGNMENTS

RESULT 1  
Q65M37\_BACLD PRELIMINARY; PRT; 307 AA.  
AC Q85M37; Q62XH4;  
DT 25-OCT-2004, integrated into UniprotKB/TREMBL.  
DT 25-OCT-2004, sequence version 1.  
DT 07-FEB-2006, entry version 15.  
DE YHCH (ABC transporter).  
GN Name=yhch; OrderedLocNames=BL03183, BL100969;  
OS Bacillus licheniformis (strain DSM 13 / ATCC 14580).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=279010;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX PubMed=1538718; DOI=10.1159/000079829;  
RA Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,  
RA Ehrenreich P., Baeumer S., Henne A., Liesegang H., Merkl R.,  
RA Ehrenreich A., Gottschalk G.;  
RT "The complete genome sequence of Bacillus licheniformis DSM13, an  
organism with great industrial potential";  
RL J. Mol. Microbiol. Biotechnol. 7:204-211(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX PubMed=15461803; DOI=10.1186/gb-2004-5-10-r77;  
RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,  
Tang M., Lopez de Leon A., Xiang H., Gusti V., Clausen I.G.,  
RA Olsen P.B., Rasmussen M.D., Andersen J.T., Joergensen P.L.,  
RA Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N.,  
RA Ehrlich S.D., Berk R.M.;  
RT "Complete genome sequence of the industrial bacterium Bacillus  
licheniformis and comparisons with closely related Bacillus species";  
RL Genome Biol. 5:RESEARCH077.1-RESEARCH077.12(2004).  
CC -1- SIMILARITY: Belongs to the ABC transporter family.  
CC Copyrighted by the Uniprot Consortium, see http://www.uniprot.org/terms  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
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CC EMBL; AE017333; AAU39877.1; -; Genomic DNA.  
CC EMBL; CP000002; AAU22534.1; -; Genomic DNA.  
CC GO; GO:0005524; F:ATP binding; IEA.  
CC GO; GO:0016887; F:ATPase activity; IEA.  
CC GO; GO:0001666; F:nucleotide binding; IEA.  
CC GO; GO:0006810; P:transport; IEA.  
CC InterPro; IPR003593; AAA\_ATPase.  
CC InterPro; IPR003439; ABC\_transp\_like.  
CC Pfam; PF00005; ABC\_tran; 1.  
CC ProDom; PD000006; ABC\_tran; 1.  
CC SMART; SM00382; AAA; 1.  
CC PROSITE; PS00211; ABC\_TRANSPORTER\_1; UNKNOWN\_1.  
CC PROSITE; PS00893; ABC\_TRANSPORTER\_2; 1.  
KW ATP-binding; Complete proteome; Nucleotide-binding; Transport.  
SQ SEQUENCE 307 AA; 34448 MW; A7ABD87C38BFBABA CRC64;

Query Match 99.9%; Score 1540; DB 2; Length 307;

[illegible]

RESULT 2

CHCH	BACSU	STANDARD;	PRT;	305 AA.
C	P54592;			
T	01-OCT-1996,	integrated into UniProtKB/Swiss-Prot.		
T	01-OCT-1996,	sequence version 1.		
T	07-MAR-2006,	entry version 41.		
E	Hyprothetical ABC transporter ATP-binding protein yhcH.			
N	Name=yhcH; OrderedLocusNames=BSU09080;			
N	Bacillus subtilis.			
S	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
C	NCBI_TaxID=1423,			
X	[1]_TaxID=1423,			
N	[1]_TaxID=1423,			
N	NUCLEOTIDE SEQUENCE [GENOMIC DNA].			
P	STRAIN=168;			
N	STRAIN=168;			
C	MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;			
X	Kunet F., Ogasawara N., Moser I., Albertini A.M., Allioni G.,			
A	Azevedo V., Bertero M.G., Bassieres P., Bolotin A., Borchert S.,			
A	Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,			
A	Brouillet S., Bruschl C.V., Caldwell B., Capuano V., Carter N.M.,			
A	Choi S.-K., Codani J.-J., Connerton I.F., Cummings N.J., Daniel R.A.,			
A	Denizot F., Devine K.M., Duesterhoeft A., Ehrlich S.D., Emmerson P.T.,			
A	Entan K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,			
A	Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,			
A	Ghim S.-Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,			
A	Guiseppi G., Guy B.J., Haga K., Hatach J., Harwood C.R., Henaut A.,			
A	Hilbert H., Holsappel S., Hosono S., Hullo M.-F., Itaya M.,			
A	Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,			
A	Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,			
A	Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,			
A	Lazarevic V., Lee S.-M., Levine A., Liu H., Masuda S., Mauel C.,			
A	Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,			
A	Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,			
A	Park S.-H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,			
A	Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,			
A	Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,			
A	Rose M., Sadaie Y., Sato T., Scantlan E., Schleich S., Schroeter R.,			

[illegible]



DT 01-MAR-2003, sequence version 1.  
 DT 21-FEB-2006, entry version 27.  
 DE ABC transporter ATP-binding protein.  
 GN OrderedLocusNames=OB1714;  
 OS Oceanobacillus thelyensis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.  
 OX NCBI\_TaxID=182710;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=HTE831 / DSM 14371 / JCM 11309;  
 RX MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526;  
 RA Takami H., Takaki Y., Uchiyama I.;  
 RT "Genome sequence of Oceanobacillus thelyensis isolated from the Iheya  
 RT Ridge and its unexpected adaptive capabilities to extreme  
 RT environments";  
 RL Nucleic Acids Res. 30:3927-3935 (2002).  
 CC -1- SIMILARITY: Belongs to the ABC transporter family.  
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 CC  
 CC EMBL; BA00028; BAC13670.1; -, Genomic DNA.  
 DR BioCyc; OHE182710:OB1714-MONOMER; -;  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0016887; F:ATPase activity; IEA.  
 DR GO; GO:0000166; F:nucleotide binding; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR003593; AAA\_ATPase.  
 DR InterPro; IPR003439; ABC\_transp\_like.  
 DR Pfam; PF00005; ABC\_tran; 1.  
 DR ProDom; PD000006; ABC\_transporter; 1.  
 DR SMART; SM00382; AAA; 1.  
 DR PROSITE; PS00211; ABC\_TRANSPORTER\_1; UNKNOWN\_1.  
 DR PROSITE; PS00893; ABC\_TRANSPORTER\_2; 1.  
 KW ATP-binding; Complete proteome; Nucleotide-binding; Transport.  
 SQ SEQUENCE 307 AA; 34261 MW; CDFBBF002C9C2F5B CRC64;  
 Query Match 52.3%; Score 806; DB 2; Length 307;  
 Best Local Similarity 51.3%; Pred. No. 1.7e-37;  
 Matches 153; Conservative 71; Mismatches 72; Indels 2; Gaps 2;  
 QY 5 LELKNVSKTIRGKKIIEGLSPDVRAGEIFGLPGNGAGKTTTIRMIVGHMSITAGEIATVC 64  
 DB 6 MELKNLSKQIKKKEIKGLNFSIERGEVFGVNGAGKTTTIRMVGLMSISGEVLQIQ 65  
 QY 65 GVSVENFEKAAKHGAIIVENPELYKFTGYQNIQQYARMTKGVTKKIDIEIVELVGLKN 124  
 DB 66 GKSTQSDYKEAIKEVGAIVENPENYPFELSGWKNLQKQFARMWPDVTDRIKSVIQLVGLK 125  
 QY 125 RINDKVITYSLGMORLGLAQLSLHDPKLLILDEPTNGLDPAQIREIRDYLRKLTREKGM 184  
 DB 126 AIHEKAGRYSLGMORLGLAQLSLHDPKLLILDEPTNGLDPAQIREIRDYLRKLTREKGM 185  
 QY 185 AVIVSSHLLSEMELMCDRIATIQNGKLRDIQHVHGPARDKKRYIQ-ADDTQALTRAA 243  
 DB 186 AVIVSSHLLTEIELMCDRIGIKNGELIAVESVRNESNKQVIQITDSDPKAQEIL 245  
 QY 244 AFR-KVKVDEAGGIEISIQKDEVPDLIKHLTDSGVRLYEYKAVNKSLEDRFLEITAD 300  
 DB 246 SGKDSLKHETSDITVNCERDEIPSLKELLNGQVLVYEVQVQVKSLEDKFFELICE 303  
 RESULT 4  
 Q61117\_BACAN  
 ID Q61117\_BACAN PRELIMINARY; PRT; 300 AA.  
 AC Q61117;  
 DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 19-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 12.  
 DE ABC transporter, ATP-binding protein.  
 GN OrderedLocusNames=BAS1274;  
 OS Bacillus anthracis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group.  
 OX NCBI\_TaxID=1392;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=Sterner;  
 RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,  
 RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,  
 RA Richardson P., Rubin E., Tice H.;  
 RT "Complete genome sequence of Bacillus anthracis Sterne";  
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: Belongs to the ABC transporter family.  
 CC  
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NoDerivs License  
 CC  
 CC EMBL; AE017225; AY53594.1; -, Genomic DNA.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0016887; F:ATPase activity; IEA.  
 DR GO; GO:0000166; F:nucleotide binding; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro; IPR003593; AAA\_ATPase.  
 DR InterPro; IPR003439; ABC\_transp\_like.  
 DR Pfam; PF00005; ABC\_tran; 1.  
 DR ProDom; PD000006; ABC\_transporter; 1.  
 DR SMART; SM00382; AAA; 1.  
 DR PROSITE; PS00211; ABC\_TRANSPORTER\_1; UNKNOWN\_1.  
 DR PROSITE; PS00893; ABC\_TRANSPORTER\_2; 1.  
 KW ATP-binding; Nucleotide-binding; Transport.  
 SQ SEQUENCE 300 AA; 33378 MW; 4FBLA80D719ACD92 CRC64;  
 Query Match 51.2%; Score 789; DB 2; Length 300;  
 Best Local Similarity 53.7%; Pred. No. 1.5e-36;  
 Matches 160; Conservative 59; Mismatches 69; Indels 10; Gaps 4;  
 QY 4 LLEKNVSKTIRGKKIIEGLSPDVRAGEIFGLPGNGAGKTTTIRMIVGHMSITAGEIATV 63  
 DB 5 VVKLENVYKKGITGGTEILIRGLSPFVREGEVYGLPGNGSGKTTTIRMVGLMSITAGEIT 64  
 QY 64 CGVSVENFEKAAKHGAIIVENPELYKFTGYQNIQQYARMT-KGVTKKIDIEIVELVGL 122  
 DB 65 CGHSIRTERKALEIQGAIIVENPELYDYMTGMQNLKHFANNAITPISKERIAEIVKLV 124  
 QY 123 KNINDKVITYSLGMORLGLAQLSLHDPKLLILDEPTNGLDPAQIREIRDYLRKLTREK 182  
 DB 125 EHAHKVITYSLGMORLGLAQLSLHDPKLLILDEPTNGLDPAQIREIRDYLRKLTREK 184  
 QY 183 GMAIVSSHLLSEMELMCDRIATIQNGKLRDIQHVHGPARDKKRYIQADDTQALTR 241  
 DB 185 NIAIVSSHLLSEIELMCDRVIIKQGEFVQYVNLHEQAKHDETIVVAVFVQVQKA--- 241  
 QY 242 AAAPRKVKVDEAGG-IELSIQKDEVPDLIKHLTDSGVRLYEYKAVNKSLEDRFLEIT 298  
 DB 242 ---NEIVQGAQGNVIVSVTKKEIPQLVKLVNNDVLVYGVTVQNKLTLEDEFLAIT 295  
 RESULT 5  
 Q6HLJ0\_BACHK  
 ID Q6HLJ0\_BACHK PRELIMINARY; PRT; 300 AA.  
 AC Q6HLJ0;  
 DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 19-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 14.  
 DE ABC transporter, ATP-binding protein; possible multidrug transporter.  
 GN Name=bcrA; OrderedLocusNames=BT9727\_1246;  
 OS Bacillus thuringiensis subsp. konkukian.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
 OC Bacillus cereus group.  
 OX NCBI\_TaxID=180856;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=97-27;  
 RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,

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RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus thuringiensis 97-27." ;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ABC transporter family.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL, A0017355; AAT59400.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0001666; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transp_like.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome; Nucleotide-binding; Transport.
SQ SEQUENCE 300 AA; 33378 MW; 4F8A80D719ACD92 CRC64;

Query Match 51.2%; Score 789; DB 2; Length 300;
Best Local Similarity 53.7%; Pred. No. 1.5e-36;
Matches 160; Conservative 59; Mismatches 69; Indels 10; Gaps 4;

QY 4 LLEKNVSTIRKGIIEGLSPDVRAGEIFGFLGPNAGKTTIRIMVGHMSITAGEIAV 63
DB 5 VVKLENVRKKGITGTEIRGLSFVEVGEVGFGLGPNAGKTTIRIMVGHMSITAGEIAV 64

QY 64 CGSVKVENPEKAARHGAIVENPELYKFLTYGNLQOYARMT-KGYTKKKKIDIVELVGL 122
DB 65 CGHSIRTEREKALEQIGAIVENPELYDYMTGMQNLKHPANMAITPISKERIAIEVKLVEL 124

QY 123 KNRINDKVITYSLGMRQRLGSLHDPKLLILDEPTNGLDPAGIREIDYLRKLTREK 182
DB 125 EHAHKKVKVITYSLGMKQRLGSLHDPKLLILDEPTNGLDPAGIREIDYLRKLTREK 184

QY 183 GMNAVIVSSHLLSEMLMCDRIALIQNGKLRDIQHVHGPAR-DEKKRYYYQADDTQALTRE 241
DB 185 NIATIVSSHLLSEMLMCDRVIIKQGEFVQEVNLEHQAKHDETVVVAFEVDQVQA--- 241

QY 242 AAARFKVKVDEAGG-IELSIQKDEVPDLIKHLTDSGVRLYEYKAVNKSLDEDFLEIT 298
DB 242 ----NEIVQKAGQNVIVSVTKEEIPQLVKLVNNDVLVYGVTVQNKLTLEDEFLAIT 295

RESULT 6
Q4MSI3_BACCE PRELIMINARY; PRT; 300 AA.
AC Q4MSI3_
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Bacitracin transport ATP-binding protein bcrA.
GN ORFNames=BCE_G9241_1372;
OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=269801;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Maiden M.C.J., Priest P.G., Barker M., Jiang L., Cer R.Z.,
RA Rillstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated
RT with an illness resembling inhalation anthrax." ;

```

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RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454 (2004).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -1- SIMILARITY: Belongs to the ABC transporter family.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL, AAEK0100009; EALJ5130.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0001666; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transp_like.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Nucleotide-binding; Transport.
SQ SEQUENCE 300 AA; 33506 MW; E0B11D19DB91DC53 CRC64;

Query Match 50.9%; Score 785; DB 2; Length 300;
Best Local Similarity 53.9%; Pred. No. 2.5e-36;
Matches 160; Conservative 55; Mismatches 74; Indels 8; Gaps 3;

QY 4 LLEKNVSTIRKGIIEGLSPDVRAGEIFGFLGPNAGKTTIRIMVGHMSITAGEIAV 63
DB 5 VVKLENVRKKGITGTEIRGLSFVEVGEVGFGLGPNAGKTTIRIMVGHMSITAGEIAV 64

QY 64 CGSVKVENPEKAARHGAIVENPELYKFLTYGNLQOYARMT-KGYTKKKKIDIVELVGL 122
DB 65 CGHSIRTEREKALEQIGAIVENPELYDYMTGMQNLKHPANMAITPISKERIAIEVKLVEL 124

QY 123 KNRINDKVITYSLGMRQRLGSLHDPKLLILDEPTNGLDPAGIREIDYLRKLTREK 182
DB 125 EHAHKKVKVITYSLGMKQRLGSLHDPKLLILDEPTNGLDPAGIREIDYLRKLTREK 184

QY 183 GMNAVIVSSHLLSEMLMCDRIALIQNGKLRDIQHVHGPAR-DEKKRYYYQADDTQALTRE 241
DB 185 NIATIVSSHLLSEMLMCDRVIIKQGEFVQEVNLEHQAKHDETVVVAFEVDQVQ----- 239

QY 242 AAARFKVKVDEAGG-IELSIQKDEVPDLIKHLTDSGVRLYEYKAVNKSLDEDFLEIT 298
DB 240 --KANEIIKKAQRNVIVSVTKEEIPQLVKLVNEDVLVYGVTVQNKLTLEDEFLAIT 295

RESULT 7
Q73BE3_BACCI PRELIMINARY; PRT; 300 AA.
AC Q73BE3_
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE ABC transporter, ATP-binding protein.
GN ORFNames=BCE_1475;
OS Bacillus cereus (strain ATCC 10987).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=222523;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=14960714; DOI=10.1093/nar/gkh258;
RA Rasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L.,
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,
RA Nelson W.C., Kolstoe A.B., Fraser C.M., Read T.D.;
RA "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic
RT adaptations and a large plasmid related to Bacillus anthracis pXO1." ;
RT Nucleic Acids Res. 32:977-988 (2004).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
CC -----

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DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR003593; AAA\_ATPase.  
DR InterPro; IPR003439; ABC\_transp\_like.  
DR GO; GO:0006810; P:transport; IEA.

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DR Pfam; PF00005; ABC tran; 1.
DR ProDom; PD000006; ABC transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome; Nucleotide-binding; Transport.
SQ SEQUENCE 300 AA; 33561 MW; 14P4E9A8CA306D53 CRC64;

Query Match 50.8%; Score 783; DB 2; Length 300;
Best Local Similarity 53.9%; Pred. No. 3.3e-36;
Matches 160; Conservative 54; Mismatches 75; Indels 8; Gaps 3;

QY 4 LLELNKVNKTIIRGKKIIIEGLSPDVRAGEIFGFLGPNAGKTTTIRMVGHMSITAGEIAV 63
   :::::::::::::::::::::
Db 5 VVKLENVRKIKGTEIIRGLSPFVREGVYGLGPNAGKTTTIRMVGHMSITAGEIAV 64
   :::::::::::::::::::::

QY 64 CGVSVKENFEKAARHIGAIVENPELYKFLTGYNLQOYARMT-KGVTKKKIDIEIVLVL 122
   :::::::::::::::::::::
Db 65 CGHSIRTEREKALEQIGAIVENPELYDYMTGMQNLKHFANMAITPIRKERIAEIVKLVEL 124
   :::::::::::::::::::::

QY 123 KNRIINDKVTYSIGMRQRLGSLAQSLHDPKLLILDEPTNGLDPAGIREIRDYLRLKLTREK 182
   :::::::::::::::::::::
Db 125 EHAHKKVKTYSLGMQRQLGIAQLLHQPKILLILDEPTNGLDPAGIRQIRDLQRLAKEE 184
   :::::::::::::::::::::

QY 183 GMAVIVSSHLLSEMELMCDRIATIQNGKLRDIQHVHGPAP-DEKKRYIYIQAADTQALTRE 241
   :::::::::::::::::::::
Db 185 NTAVIVSSHLLSEIELMCDRVVIKQGEFVQVYNLHEQAKHDETVVVAPEVDQVQ---- 239

QY 242 AAAPRVKVDVDEAGG-IELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSIEDRFLFIT 298
   :::::::::::::::::::::
Db 240 -KANEIIGKAQRNVIVSVTKTEIIPQLVKLVNDVLYGVTVQNKLTLEDEFLAIT 295

RESULT 10
Q8IGS1_BACCR PRELIMINARY; PRT; 300 AA.
AC Q8IGS1;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Bacitracin transport ATP-binding protein bcrA.
GN OrderedLocusNames=BC1359; ORFNames=BC_1359;
OS Bacillus cereus (strain ATCC 14579 / DSM 31).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=226900;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582;
RX Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
RA Kapatal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
RA Chu L., Mazur M., Goltzman E., Larsen N., D'Souza M., Walunas T.,
RA Grechkin Y., Puech G., HaeselKorn R., Fonstein M., Ehrlich S.D.,
RA Overbeek R., Kyrpides N.C.;
RT "Genome sequence of Bacillus cereus and comparative analysis with
   Bacillus anthracis."
RL Nature 423:87-91(2003).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
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CC -----
CC EMBL; AE016877; AAP08341.1; -; Genomic_DNA.
DR BLOCYC; BCER226900.BC1359-MONOMER; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0001666; F:nucleotide binding; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transp_like.
DR Pfam; PF00005; ABC tran; 1.
DR ProDom; PD000006; ABC transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome; Nucleotide-binding; Transport.
SQ SEQUENCE 300 AA; 33561 MW; 14P4E9A8CA306D53 CRC64;

Query Match 50.6%; Score 781; DB 2; Length 300;
Best Local Similarity 53.4%; Pred. No. 4.2e-36;
Matches 159; Conservative 57; Mismatches 72; Indels 10; Gaps 4;

QY 4 LLELNKVNKTIIRGKKIIIEGLSPDVRAGEIFGFLGPNAGKTTTIRMVGHMSITAGEIAV 63
   :::::::::::::::::::::
Db 5 VVKLENVRKIKGTEIIRGLSPFVREGVYGLGPNAGKTTTIRMVGHMSITAGEIAV 64
   :::::::::::::::::::::

QY 64 CGVSVKENFEKAARHIGAIVENPELYKFLTGYNLQOYARMT-KGVTKKKIDIEIVLVL 122
   :::::::::::::::::::::
Db 65 CGHSIRTEREKALEQIGAIVENPELYDYMTGMQNLKHFANMAITPIRKERIAEIVKLVEL 124
   :::::::::::::::::::::

QY 123 KNRIINDKVTYSIGMRQRLGSLAQSLHDPKLLILDEPTNGLDPAGIREIRDYLRLKLTREK 182
   :::::::::::::::::::::
Db 125 EHAHKKVKTYSLGMQRQLGIAQLLHQPKILLILDEPTNGLDPAGIRQIRDLQRLAKEE 184
   :::::::::::::::::::::

QY 183 GMAVIVSSHLLSEMELMCDRIATIQNGKLRDIQHVHGPAP-DEKKRYIYIQAADTQALTRE 241
   :::::::::::::::::::::
Db 185 NTAVIVSSHLLSEIELMCDRVVIKQGEFVQVYNLHEQAKHDETVVVAPEVDQVQ---- 241

QY 242 AAAPRVKVDVDEAGG-IELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSIEDRFLFIT 298
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Db 242 ----NEIIGKAGKNVIVSVTKDNIPQLVKLVHADVLVYGVTVQNKLTLEDEFLAIT 295

RESULT 11
Q6HAN5_BACHK PRELIMINARY; PRT; 305 AA.
AC Q6HAN5;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE ABC transporter, ATP-binding protein; possible bacitracin transport
   ATP-binding protein.
DE ATP-binding protein.
GN OrderedLocusNames=BT9727.5081;
OS Bacillus thuringiensis subsp. konkukian.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=180856;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=97-27;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RL "Complete genome sequence of Bacillus thuringiensis 97-27."
CC Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ABC transporter family.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; AE017355; AAT62644.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0016887; F:ATPase activity; IEA.
DR GO; GO:0001666; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transp_like.
DR Pfam; PF00005; ABC tran; 1.
DR ProDom; PD000006; ABC transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
KW ATP-binding; Complete proteome; Nucleotide-binding; Transport.
SQ SEQUENCE 305 AA; 34326 MW; 92E123A0CBC4D0D7 CRC64;

Query Match 48.9%; Score 754.5; DB 2; Length 305;
Best Local Similarity 48.2%; Pred. No. 1.3e-34;
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RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RX PubMed=14960714; DOI=10.1093/nar/gkh259;  
RA Rasko D.A., Ravel J., Osekstad O.A., Helgason E., Cer R.Z., Jiang L.,  
RA Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F.,  
RA Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;  
RT "The genome sequence of *Bacillus cereus* ATCC 10987 reveals metabolic  
RT adaptations and a large plasmid related to *Bacillus anthracis* pXO1.";  
RL Nucleic Acids Res. 32:977-988(2004).  
CC -!- SIMILARITY: Belongs to the ABC transporter family.  
-----  
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms  
CC Distributed under the Creative Commons Attribution-NoDerivs License  
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CC EMBL; AS017194; AA544429.1; -: Genomic\_DNA.  
DR GO; GO:0005524; P:ATP binding; IEA.  
DR GO; GO:0016987; F:ATPase activity; IEA.  
DR GO; GO:0016676; F:nucleotide binding; IEA.  
DR InterPro; IPR003593; AAA\_ATPase.  
DR IntesPro; IPR003439; ABC\_transp\_like.  
DR Pfam; PF00005; ABC\_tran; 1.  
DR PRODom; PD000006; ABC\_transporter; 1.  
DR SMART; SM00382; AAA\_1.  
DR PROSITE; PS00211; ABC\_TRANSPORTER\_1; UNKNOWN\_1.  
DR PROSITE; PS00893; ABC\_TRANSPORTER\_2; 1.  
KW ATP-binding; Complete proteome; Nucleotide-binding; Transport.  
SQ SEQUENCE 305 AA; 34406 MW; FDEEA942E1DFF99A CRC64;

Query Match 48.2%; Score 743.5; DB 2; Length 305;  
Best Local Similarity 47.8%; Pred. No. 5.5e-34;  
Matches 150; Conservative 68; Mismatches 77; Indels 19; Gaps 3

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1 MTIILSVRDVKKVIKNKTLVENISFDTQGEVFGLPGNGAGKTTTIRMLVLGIKATEGT 60  
QY 61 IAVGVSVKENPFKAARHICAIVENPELYKFLTCYQNLOQYARMTKGVTKKKIDIVELV 120  
DB :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
61 ISIGYSIKENFREARMRQGISVENPELYTLTGWENLKQPARMLGDISDIRIMEIAQM 120  
QY 121 GLANRNNDKVTVSLGNQRQLGAQSLLHPDKLLILDPTNLGPAGIREIRDYLRLKLT 180  
DB |||DLRIHDKVTYSLGNKQRGLTAQALLGNPKLLILDPTNLGPAGIREIRFIHLVK 180  
QY 181 EKMMAVIVSHLLSEMELMCDRIAIIQNGKLRIQHVGPARDEKKRY-YIQADDTQALT 239  
DB :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
181 EENNSVFISILLSEVQMICDRVAIIHKGMITVAKVEELIKITASDRVEMIVTPIGKA-- 238  
QY 240 REAAAFKVKVDNREGGIELSIQKD-----EVPDLIKHLTDSGVRLEVYKAVNKSL 290  
DB |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
239 -----KMLEDAEBEVREVSIEGRULLCRMNIASINWNKHFEVNEIDVHSVKELVFTL 291  
QY 291 EDRLFLEITADKEEA 304  
DB |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:  
292 EDLFIELTRCEQHA 305

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AC Q4MLR2;  
DT 02-AUG-2005, integrated into UniProtKB/TREMBL.  
DT 02-AUG-2005, sequence version 1.  
DT 07-FEB-2006, entry version 7.  
DE Bacitracin transport ATP-binding protein bcrA.  
OS ORFNAMES=BCE G9241\_5584;  
GN *Bacillus cereus* G9241.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC *Bacillus cereus* group.  
OX NCBI\_TaxID=269801;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=G9241;  
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;

QAMLR2,  
02-AUG-2005, integrated into UniProtKB/TrEMBL.  
02-AUG-2005, sequence version 1.  
07-FEB-2006, entry version 7.  
DE Bacitracin transport ATP-binding protein bcrA.  
GN ORFNames=BCE G9241\_5584;  
OS Bacillus cereus G9241.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;  
OC Bacillus cereus group.  
OX NCBI\_taxid=269801;  
[1]  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=G9241;  
RC PubMed=15155910; DOI=10.1073/pnas.0402414101;  
RX





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OM protein - protein search, using sw model

Run on: July 13, 2006, 13:49:18 ; Search time 50 Seconds  
(without alignments)  
537.438 Million cell updates/sec

Title: US-10-510-941-2  
Perfect score: 1542  
Sequence: 1 LETLLEKNVSKTIRGKKII.....KSLEDRFLTEADKERAQHV 307.

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

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- 2: /EMC\_Celerra\_SID33/ptodata/2/iaa/6 COMB.pdp.\*
- 3: /EMC\_Celerra\_SID33/ptodata/2/iaa/7 COMB.pdp.\*
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- 5: /EMC\_Celerra\_SID33/ptodata/2/iaa/PTCTUS COMB.pdp.\*
- 6: /EMC\_Celerra\_SID33/ptodata/2/iaa/RE COMB.pdp.\*
- 7: /EMC\_Celerra\_SID33/ptodata/2/iaa/baCKfilese1.pdp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	455.5	29.5	310	2	US-09-107-532A-6910
2	436	28.3	233	2	US-09-627-376-12
3	436	28.3	233	2	US-10-047-676B-12
4	430.5	27.9	332	2	US-09-107-532A-3752
5	416.5	27.0	303	2	US-09-107-532A-5192
6	410	26.6	345	2	US-09-252-991A-31957
7	408.5	26.5	330	2	US-09-902-540-15345
8	407.5	26.4	319	2	US-09-758-759-89
9	397	25.7	328	2	US-09-902-540-10796
10	396.5	25.7	309	2	US-09-252-991A-21204
11	392.5	25.5	215	2	US-09-583-110-2846
12	392.5	25.5	229	2	US-09-107-433-3116
13	391.5	25.4	309	2	US-09-902-540-16586
14	384.5	24.9	228	2	US-09-602-787A-402
15	381	24.7	788	2	US-09-252-991A-28171
16	374.5	24.3	240	2	US-09-902-540-15786
17	373	24.2	292	2	US-09-602-787A-352
18	371.5	24.1	290	2	US-09-902-540-16248
19	371.5	24.1	594	2	US-09-543-681A-5528
20	367	23.8	588	2	US-09-489-039A-13579
21	363.5	23.6	315	2	US-09-134-000C-6449
22	362.5	23.5	245	2	US-09-902-540-13001
23	354.5	23.0	248	2	US-09-710-279-3218
24	352.5	22.9	316	2	US-09-902-540-10994
25	349.5	22.7	1272	2	US-09-949-016-7472
26	347.5	22.5	2059	3	US-10-114-270-176

27	347.5	22.5	2144	2	US-10-154-419-2	Sequence 2, Appli
28	347.5	22.5	2146	2	US-09-949-016-6947	Sequence 6947, Ap
29	346.5	22.5	1684	2	US-08-665-259-25	Sequence 25, Appl
30	346.5	22.5	1684	2	US-08-762-500-25	Sequence 25, Appl
31	346.5	22.5	1704	2	US-08-762-500-75	Sequence 75, Appl
32	346.5	22.5	1704	2	US-09-032-438C-120	Sequence 120, App
33	346.5	22.5	1766	2	US-09-949-016-10796	Sequence 10796, A
34	345.5	22.4	304	2	US-09-107-532A-5424	Sequence 5424, Ap
35	344.5	22.3	607	2	US-09-252-991A-18351	Sequence 18351, A
36	344	22.3	257	2	US-09-107-532A-4066	Sequence 4066, Ap
37	342.5	22.2	205	2	US-09-134-001C-4766	Sequence 4766, Ap
38	341.5	22.1	254	2	US-09-107-532A-4983	Sequence 4983, Ap
39	341	22.1	291	2	US-09-107-532A-4205	Sequence 4205, Ap
40	340	22.0	323	2	US-09-489-039A-12496	Sequence 12496, A
41	339.5	22.0	589	2	US-09-328-352-7592	Sequence 7592, Ap
42	339	22.0	317	2	US-09-583-110-5279	Sequence 5279, Ap
43	339	22.0	327	2	US-09-107-433-3331	Sequence 3331, Ap
44	335	21.7	315	2	US-09-328-352-4388	Sequence 4388, Ap
45	334.5	21.7	2273	2	US-09-032-438C-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-09-107-532A-6910  
; Sequence 6910, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD/ROM ISO9660  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107.532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 6910:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 310 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (B) LOCATION 1...310  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6910:

## US-09-107-532A-6910

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Best Local Similarity 34.6%; Pred. No. 7.2e-36;  
Matches 104; Conservative 79; Mismatches 107; Indels 11; Gaps 6;  
  
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QY 62 AVCGSVKVFENFEKAARHIGAIVENPELYKFLTYQNLQOYARMTKVTGKKKIDEIVELVG 121  
DB 71 ELFGTT--DLQAARRMGQSIETPALYPELTARDNLRIQA-ANGGVSDREIBDLKQMR 126  
  
QY 122 LKNRINDKVTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRYLRKLTR 181  
DB 127 LENTGKKKAKNFSGLMRQRLAIANALITNPEFLIDEPNTGMDPAGMAENREIQRVLKE 186  
  
QY 182 KGMVIVSSHLLSEMELMCDRIAIIONGKLRDIOHVHGPARDKRYIYQADPT---QAL 238  
DB 187 RGITVLLSSHLDELQIATHYGLHEGL--IKELSKBELAQESQFIKIDTSATEQAV 244  
  
QY 239 T-REAAAFKVKVDEAGGIELSIQKDEVPDLIKHLTDSGVRLYEYKAVNKSLEDRLFEI 297  
DB 245 TVLDSLGYRDYFV-QSSRVQLFEGIDQVAAINQALVEAKVPVDGHLVQKLEDFLOL 303  
  
QY 298 T 298  
DB 304 T 304

## RESULT 2

US-09-627-376-12  
; Sequence 12, Application US/09627376

; Patent No. 6342385

; GENERAL INFORMATION:

; APPLICANT: Qi, Fengxia Caufield, Page Chen, Ping

; TITLE OF INVENTION: MUTACIN I BIOSYNTHESIS GENES AND PROTEINS

; FILE REFERENCE: UAB-17402/22

; CURRENT APPLICATION NUMBER: US/09/627,376

; CURRENT FILING DATE: 2001-05-30

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 12

; LENGTH: 233

; TYPE: PRT

; ORGANISM: Streptococcus mutans

US-09-627-376-12

Query Match 28.3%; Score 436; DB 2; Length 233;  
Best Local Similarity 41.5%; Pred. No. 3.7e-34;  
Matches 93; Conservative 51; Mismatches 72; Indels 8; Gaps 4;

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QY 61 IAVCGSVKVFENFEKAARHIGAIVENPELYKFLTYQNLQOYARMTKVTGKKKIDEIVELV 120  
DB 61 ILIDG---HDWSRKDLNIGALIESPPLYENLTARENKVRTLM-GLPDSRIDEVLKIV 116  
  
QY 121 GLKNRINDKVTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRYLRKLTR 180  
DB 117 DLNTGKKRAGQFSMGKQRLGIAIALNSPQLILDEPTNGLDPGIGQLRNLIRSFT 176  
  
QY 181 EKMVAVIVSSHLLSEMELMCDRIAIIONGKLRDIOHVHGPARD 224  
DB 177 Q-GITVIISHSILSEIQMTADHIGIANGVLGYQDRIH---QDE 216

## RESULT 3

US-10-047-676B-12

; Sequence 12, Application US/10047676B

; Patent No. 6699970  
; GENERAL INFORMATION:  
; APPLICANT: Qi, Fengxia  
; APPLICANT: Caufield, Page W.  
; APPLICANT: Chen, Ping  
; TITLE OF INVENTION: MUTACIN I BIOSYNTHESIS GENES AND PROTEINS  
; FILE REFERENCE: UAB-17403/22  
; CURRENT APPLICATION NUMBER: US/10/047,676B  
; CURRENT FILING DATE: 2002-01-14  
; PRIOR APPLICATION NUMBER: US 09/627,376  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 12  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Streptococcus mutans  
US-10-047-676B-12

Query Match 28.3%; Score 436; DB 2; Length 233;  
Best Local Similarity 41.5%; Pred. No. 3.7e-34;  
Matches 93; Conservative 51; Mismatches 72; Indels 8; Gaps 4;  
  
QY 1 LETLLEKLVKVTIRGKKIIEGLSFDVRAGEIFGLGPNAGAGKTTTIRMIVGHMSITAGE 60  
DB 1 MDYMLETKNLTKQFGKQTAVNQLNKKVERHSIYGLLGPNGSGKSTTLKMITGMLRKTSGH 60  
  
QY 61 IAVCGSVKVFENFEKAARHIGAIVENPELYKFLTYQNLQOYARMTKVTGKKKIDEIVELV 120  
DB 61 ILIDG---HDWSRKDLNIGALIESPPLYENLTARENKVRTLM-GLPDSRIDEVLKIV 116  
  
QY 121 GLKNRINDKVTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAGIREIRYLRKLTR 180  
DB 117 DLNTGKKRAGQFSMGKQRLGIAIALNSPQLILDEPTNGLDPGIGQLRNLIRSFT 176  
  
QY 181 EKMVAVIVSSHLLSEMELMCDRIAIIONGKLRDIOHVHGPARD 224  
DB 177 Q-GITVIISHSILSEIQMTADHIGIANGVLGYQDRIH---QDE 216

## RESULT 4

US-09-107-532A-3752  
; Sequence 3752, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012



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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31957

Query Match          26.6%; Score 410; DB 2; Length 345;
Best Local Similarity 29.5%; Pred. No. 2.2e-31;
Matches 94; Conservative 77; Mismatches 116; Indels 32; Gaps 6;

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Db 36 ETWIDIRLSKRFSGRTVVNDLSFRIDRGEIVGLLGNAGKSTTLKMLSGFLAPSAGSV 95

QY 62 AVCVSVKENFEKAAHIGAIVENPELY-----KELTGYQNLQOYARMTKGVTKKIDB 115
Db 96 RIFGFMQDKARQAQLKGLYPENAFSYGEMTVGEFLAFVAFVIRDSYSGREK---RRRIDS 152

QY 116 IVELVLGNRINDKVKTSYSGMRQRLGSLAQLHDPKLLILDPTNGLDPAGIREIRDYL 175
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Db 213 KNLSESK--IVVISTHILEEVSFMCSEALVINGRLL-ADNTPGELRTRSRVHHAVLSLI 269

QY 236 QALTREAAAFKRVKVVDEAEG-----GIELSQKDEVPDLIKHLTDSGVRLY 281
Db 270 EAPVDPPLAIAMLPGVAGIEGRPDRAAGTTLTILAPGVQI-----LPALNRLIHGSGWRVS 323

QY 282 EVKAVNKSLEDRFLEITAD 300
Db 324 GVRTEHQLEEVFRQLTRE 342

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; Query Match          26.4%; Score 407.5; DB 2; Length 319;
; Best Local Similarity 32.0%; Pred. No. 3.4e-31;
; Matches 101; Conservative 65; Mismatches 125; Indels 25; Gaps 8;
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15345
; TYPE: PR
; ORGANISM: Myxococcus xanthus
US-09-502-540-15345

Query Match          26.5%; Score 408.5; DB 2; Length 330;
Best Local Similarity 31.5%; Pred. No. 2.9e-31;
Matches 100; Conservative 71; Mismatches 109; Indels 37; Gaps 7;

QY 2 ETLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAGEI 61
Db 12 QPLLQLEGLTRFRFGKRTAVDGLSVRPGIEILGLLGNAGKSTTFQVLGAGLSDPAGLV 71

QY 62 AVCVSVKENFEKAAHIGAIVENPELYKFLTGYQNLQOYARMTKGV---TKKKIDEIV 117
Db 72 RFEGRELSGDSPLSRQNGIIFORSSLDLLTARENLMGARL-YLGGGERARERVEAML 130

QY 118 ELVGLKNRINDKVKTSYSLGMRQRLGSLAQLHDPKLLILDPTNGLDPAGIREIRDYLR 177
Db 131 SLIGLADRGDERVSTWGGMRRLLELARALVHQPRVLLMDPTQGLDEAAFRFTWAHLKR 190

QY 178 LTRKGMNAVIVSSHLLSEMELMCDRIAIIQNGKLRDIOHVHGPARDEKRYIIQ 223
Db 191 LRDSSEGLTVLLTTHRADEAD-VCORLAVDAGKLVACDTPQALASRWGGDILSV----- 243

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31957

Query Match          26.6%; Score 410; DB 2; Length 345;
Best Local Similarity 29.5%; Pred. No. 2.2e-31;
Matches 94; Conservative 77; Mismatches 116; Indels 32; Gaps 6;

QY 2 ETLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAGEI 61
Db 36 ETWIDIRLSKRFSGRTVVNDLSFRIDRGEIVGLLGNAGKSTTLKMLSGFLAPSAGSV 95

QY 62 AVCVSVKENFEKAAHIGAIVENPELY-----KELTGYQNLQOYARMTKGVTKKIDB 115
Db 96 RIFGFMQDKARQAQLKGLYPENAFSYGEMTVGEFLAFVAFVIRDSYSGREK---RRRIDS 152

QY 116 IVELVLGNRINDKVKTSYSGMRQRLGSLAQLHDPKLLILDPTNGLDPAGIREIRDYL 175
Db 153 AMDCMELURDERRIETLSGKFRVVALAQAILHDPKLLILDPTNGLDPAGIREIRDYL 212

QY 176 RKLTRKGMNAVIVSSHLLSEMELMCDRIAIIQNGKLRDIOHVHGPARDEKRYIIQADDT 235
Db 213 KNLSESK--IVVISTHILEEVSFMCSEALVINGRLL-ADNTPGELRTRSRVHHAVLSLI 269

QY 236 QALTREAAAFKRVKVVDEAEG-----GIELSQKDEVPDLIKHLTDSGVRLY 281
Db 270 EAPVDPPLAIAMLPGVAGIEGRPDRAAGTTLTILAPGVQI-----LPALNRLIHGSGWRVS 323

QY 282 EVKAVNKSLEDRFLEITAD 300
Db 324 GVRTEHQLEEVFRQLTRE 342

RESULT 8
US-09-758-759-89
; Query Match          26.4%; Score 407.5; DB 2; Length 319;
; Best Local Similarity 32.0%; Pred. No. 3.4e-31;
; Matches 101; Conservative 65; Mismatches 125; Indels 25; Gaps 8;
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: ID0983K US
; CURRENT APPLICATION NUMBER: US/09/758,759
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/175,751
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 89
; LENGTH: 319
; TYPE: PR
; ORGANISM: Micromonospora carbonacea
; FEATURE:
; OTHER INFORMATION: evbc
US-09-758-759-89

Query Match          26.4%; Score 407.5; DB 2; Length 319;
Best Local Similarity 32.0%; Pred. No. 3.4e-31;
Matches 101; Conservative 65; Mismatches 125; Indels 25; Gaps 8;

QY 4 LLELKNVSKTIRGK-----KIIEGLSFDVRAGEIFGFLGPNAGKTTTIRMIVGHMS 55
Db 1 MIQTRGLRKSFRSRAGRQHKTVDAVRGVLDVAEGEIFGFLGPNAGKTTTIRMIVGHMS 60

QY 56 ITAGEIACVGSVKENFEKAAHIGAIVENPELYKFLTGYQNLQOYARMTKGVTK---K 111
Db 61 PDGGQATIAAGADLLRNPAEVRRIIGYVAQGGSTWDSTAREELVLTARM-YGIGKADALR 119

QY 112 KIDEIVELVGLKNRINDKVKTSYSLGMRQRLGSLAQLHDPKLLILDPTNGLDPAGIREI 171
Db 120 RAERLAAAFQLTEYADRKCKTYSGGQRRVVEALGIIHDPRIVFLDEPTSGLDPSRAHM 179

QY 172 RDLRKLTRKGMNAVIVSSHLLSEMELMCDRIAIIQNGKLRDIOHVHGPARDEKRYIIQ 231
Db 180 WDEIRRL-RAEGMTVFITTHYLDEADALCDRIAIMDHGEVAVAGTGPGLKREISGEVLLV 238

QY 232 ADDTQALTREAAAFKRVKVVDEAEG-----KELTGYQNLQOYARMTKGVTK---K 282
Db 239 GLDA-AATPQAAQLDTEPYVTKLETVDGG-GLRLTVDEGATAIPQVLRRLDQSGURLSS 296

QY 283 KVAVNKSLEDRFLEIT 298
Db 297 IELHRSLODVLTKT 312

RESULT 9
US-09-902-540-10796
; Query Match          26.4%; Score 407.5; DB 2; Length 319;
; Best Local Similarity 32.0%; Pred. No. 3.4e-31;
; Matches 101; Conservative 65; Mismatches 125; Indels 25; Gaps 8;
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: ID0983K US
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/175,751
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 89
; LENGTH: 319
; TYPE: PR
; ORGANISM: Micromonospora carbonacea
; FEATURE:
; OTHER INFORMATION: evbc
US-09-902-540-10796

Query Match          26.4%; Score 407.5; DB 2; Length 319;
Best Local Similarity 32.0%; Pred. No. 3.4e-31;
Matches 101; Conservative 65; Mismatches 125; Indels 25; Gaps 8;

QY 4 LLELKNVSKTIRGK-----KIIEGLSFDVRAGEIFGFLGPNAGKTTTIRMIVGHMS 55
Db 1 MIQTRGLRKSFRSRAGRQHKTVDAVRGVLDVAEGEIFGFLGPNAGKTTTIRMIVGHMS 60

QY 56 ITAGEIACVGSVKENFEKAAHIGAIVENPELYKFLTGYQNLQOYARMTKGVTK---K 111
Db 61 PDGGQATIAAGADLLRNPAEVRRIIGYVAQGGSTWDSTAREELVLTARM-YGIGKADALR 119

QY 112 KIDEIVELVGLKNRINDKVKTSYSLGMRQRLGSLAQLHDPKLLILDPTNGLDPAGIREI 171
Db 120 RAERLAAAFQLTEYADRKCKTYSGGQRRVVEALGIIHDPRIVFLDEPTSGLDPSRAHM 179

QY 172 RDLRKLTRKGMNAVIVSSHLLSEMELMCDRIAIIQNGKLRDIOHVHGPARDEKRYIIQ 231
Db 180 WDEIRRL-RAEGMTVFITTHYLDEADALCDRIAIMDHGEVAVAGTGPGLKREISGEVLLV 238

QY 232 ADDTQALTREAAAFKRVKVVDEAEG-----KELTGYQNLQOYARMTKGVTK---K 282
Db 239 GLDA-AATPQAAQLDTEPYVTKLETVDGG-GLRLTVDEGATAIPQVLRRLDQSGURLSS 296

QY 283 KVAVNKSLEDRFLEIT 298
Db 297 IELHRSLODVLTKT 312
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; NUMBER OF SEQUENCES: 5206  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
 ; STREET: 100 Beaver Street  
 ; CITY: Waltham  
 ; STATE: Massachusetts  
 ; COUNTRY: USA  
 ; ZIP: 02354  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: CD/ROM ISO9660  
 ; COMPUTER: <Unknown>  
 ; OPERATING SYSTEM: <Unknown>  
 ; SOFTWARE: <Unknown>  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/107,433  
 ; FILING DATE: 30-Jun-1998  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/ 085131  
 ; FILING DATE: May 12, 1998  
 ; APPLICATION NUMBER: 60/051553  
 ; FILING DATE: July 2, 1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Ariniello, Pamela Deneke  
 ; REGISTRATION NUMBER: 40,489  
 ; REFERENCE/DOCKET NUMBER: GTC-011  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (781)893-5007  
 ; TELEFAX: (781)893-8277  
 ; INFORMATION FOR SEQ ID NO: 3116:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 229 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; HYPOTHETICAL: YES  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Streptococcus pneumoniae  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (B) LOCATION 1...229  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3116:  
 ; US-09-107-433-3116

Query Match 25.5%; Score 392.5; DB 2; Length 229;  
 Best Local Similarity 33.7%; Pred. No. 6e-30;  
 Matches 70; Conservative 62; Mismatches 75; Indels 1; Gaps 1;  
 QY 1 LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAGE 60  
 Db 15 MNEIITLKNIELKTKTCVFNLFCKQGEIIGTGANGSGKSVLFKLIAGLYSPSYGE 74  
 QY 61 IAVCGSVKNEFKAARHIGAIVENPELYKFLTGYNLQOYARMTKGVTKKIDEIVELV 120  
 Db 75 VLINGENIVPE-RKIPANLGALEEFGFINYSFGFNQLQYLASIRGVVGQCEINDTLKIV 133  
 QY 121 GLKNRINDVKYTSGLNRQRLGLAQLSLHDPKLLILDPTNGLDPAGIREIRDLRLKLR 180  
 Db 134 GLVEQKQDKVYTSGLNRKLLGLTAQAIMENPSTILLDDPNALDKSVENWRTLFRLKLS 193  
 QY 181 EKGNAVIVSHLLSEMELMCDRIAION 208  
 Db 194 EKGTTILIASHSBEDIRILCDKVAIED 221

RESULT 13  
 US-09-902-540-16586  
 ; Sequence 16586, Application US/09902540  
 ; Patent No. 6833447  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Goldman, Barry S.  
 ; APPLICANT: Hinkle, Gregory J.  
 ; APPLICANT: Slater, Steven C.  
 ; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
 ; FILE REFERENCE: 38-10(15849)B  
 ; CURRENT APPLICATION NUMBER: US/09/902,540  
 ; CURRENT FILING DATE: 2001-07-10  
 ; PRIOR APPLICATION NUMBER: 60/217,883  
 ; PRIOR FILING DATE: 2000-07-10  
 ; NUMBER OF SEQ ID NOS: 16825  
 ; SEQ ID NO 16586  
 ; LENGTH: 309  
 ; TYPE: PRT  
 ; ORGANISM: Myxococcus xanthus  
 ; US-09-902-540-16586  
 Query Match 25.4%; Score 391.5; DB 2; Length 309;  
 Best Local Similarity 32.8%; Pred. No. 1.2e-29;  
 Matches 105; Conservative 62; Mismatches 118; Indels 35; Gaps 9;  
 QY 4 LLELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAGEIAV 63  
 Db 1 MIQVEGLTKYGEHAARELAFTISQGEVIGFLGLNGAGKSTTLKVLGCVLMPTSGRWVI 60  
 QY 64 CGVSVKNEFKAARHIGAIVENPELYKFLTGYNLQOYARMTKGVTKK----KIDEIVEL 119  
 Db 61 DGHVVSNNAHEVRQRIGYLPDPVPLDYDENTVGEYL--TYVAQLRGVTSRDTASRVGEAEK 119  
 QY 120 VGLKNRINDVKYTSGLMRQRLGLAQLSLHDPKLLILDPTNGLDPAGIREIRDLRLKLT 179  
 Db 120 TGLRDVHGEIISTLSHGVRQVRGVAQALVHKPALLILDEPTSLGDRQIVEMRDVIRGL- 178  
 QY 180 REKGM-AVIVSSHLLSEMELMCDRIAIONG-----KLRDIQHVHGPARDEK 225  
 Db 179 --KGATVILVSSHILPEISQTCDRLLIHKMLMVAOGTEELAAKNGRGTILEVRGDK 236  
 QY 226 KRYVIQADDTQALTREAAAFKRVKVDAREGG-IELSIQ--KDEVPLIKHLTDSGVRLYE 282  
 Db 237 AR-----AVEVLQR----FGSVEVDASDGLVALTVRASPDQRPQVAQVVGAGLELLR 286  
 QY 283 VKAVNKSLEDRFLEITADKE 302  
 Db 287 LDQGAGQLESIFLRLTHGQE 306  
 RESULT 14  
 US-09-602-787A-402  
 ; Sequence 402, Application US/09602787A  
 ; Patent No. 6696561  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pompejus, Mark  
 ; APPLICANT: Kruger, Burkhard  
 ; APPLICANT: Schuder, Hartwig  
 ; APPLICANT: Zelder, Oskar  
 ; APPLICANT: Haberhauer, Gregor  
 ; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
 ; TITLE OF INVENTION: INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE  
 ; TITLE OF INVENTION: TRANSPORT  
 ; FILE REFERENCE: EGI-125CP  
 ; CURRENT APPLICATION NUMBER: US/09/602,787A  
 ; CURRENT FILING DATE: 2000-06-23  
 ; PRIOR APPLICATION NUMBER: USSN 60/141031  
 ; PRIOR FILING DATE: 1999-06-25  
 ; PRIOR APPLICATION NUMBER: DE 19931454.3  
 ; PRIOR FILING DATE: 1999-07-08  
 ; PRIOR APPLICATION NUMBER: DE 19931478.0  
 ; PRIOR FILING DATE: 1999-07-08  
 ; PRIOR APPLICATION NUMBER: DE 19931563.9  
 ; PRIOR FILING DATE: 1999-07-08  
 ; PRIOR APPLICATION NUMBER: DE 19932122.1  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: DE 19932124.8  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: DE 19932125.6  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: DE 19932128.0

; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: DE 19932180.9  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: DE 19932182.5  
 ; PRIOR FILING DATE: 1999-07-09  
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 ; PRIOR FILING DATE: 1999-07-09  
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 ; PRIOR FILING DATE: 1999-07-09  
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 ; PRIOR FILING DATE: 1999-07-09  
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 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: DE 19932228.7  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: DE 19932229.5  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: DE 19932230.9  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: DE 19932927.3  
 ; PRIOR FILING DATE: 1999-07-14  
 ; PRIOR APPLICATION NUMBER: DE 19933005.0  
 ; PRIOR FILING DATE: 1999-07-14  
 ; PRIOR APPLICATION NUMBER: DE 19933006.9  
 ; PRIOR FILING DATE: 1999-07-14  
 ; PRIOR APPLICATION NUMBER: DE 19940764.9  
 ; PRIOR FILING DATE: 1999-08-27  
 ; PRIOR APPLICATION NUMBER: DE 19940765.7  
 ; PRIOR FILING DATE: 1999-08-27  
 ; PRIOR APPLICATION NUMBER: DE 19940766.5  
 ; PRIOR FILING DATE: 1999-08-27  
 ; PRIOR APPLICATION NUMBER: DE 19940830.0  
 ; PRIOR FILING DATE: 1999-08-27  
 ; PRIOR APPLICATION NUMBER: DE 19940831.9  
 ; PRIOR FILING DATE: 1999-08-27  
 ; PRIOR APPLICATION NUMBER: DE 19940832.7  
 ; PRIOR FILING DATE: 1999-08-27  
 ; PRIOR APPLICATION NUMBER: DE 19940833.5  
 ; PRIOR FILING DATE: 1999-08-27  
 ; PRIOR APPLICATION NUMBER: DE 19941378.9  
 ; PRIOR FILING DATE: 1999-08-31  
 ; PRIOR APPLICATION NUMBER: DE 19941379.7  
 ; PRIOR FILING DATE: 1999-08-31  
 ; PRIOR APPLICATION NUMBER: DE 19941395.9  
 ; PRIOR FILING DATE: 1999-08-31  
 ; PRIOR APPLICATION NUMBER: DE 19942077.7  
 ; PRIOR FILING DATE: 1999-09-03  
 ; PRIOR APPLICATION NUMBER: DE 19942078.5  
 ; PRIOR FILING DATE: 1999-09-03  
 ; PRIOR APPLICATION NUMBER: DE 19942079.3  
 ; PRIOR FILING DATE: 1999-09-03  
 ; PRIOR APPLICATION NUMBER: DE 19942088.2  
 ; PRIOR FILING DATE: 1999-09-03  
 ; NUMBER OF SEQ ID NOS: 678  
 ; SEQ ID NO 402  
 ; LENGTH: 228  
 ; TYPE: PRT  
 ; ORGANISM: Corynebacterium glutamicum  
 US-09-602-787A-402

Query Match 24.9%; Score 384.5; DB 2; Length 228;  
 Best Local Similarity 41.2%; Pred. No. 3.6e-29;  
 Matches 87; Conservative 45; Mismatches 70; Indels 9; Gaps 4;  
 Qy 4 LLEKNVSKTIRGKIIIEGLSPDVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAGEIAV 63  
 Db 1 MINVEGLTKYQGVQRAVDLSPFVKGIIVTGFGLGPNAGKSTTWRLLGLDNFTAGUATI 60  
 Qy 64 CGV---SVKENFEKAARHGAIVENPELYKFLTGYNLOQYARMKGVTKKKIDEIVELV 120  
 Db 61 EGOPYRSLKNPLTK---VQALLDAKATHNRTAENHLKWIAR-ANGLSTKRVDEVLTAV 115

Qy 121 GLKVRINDKVTYSIGMRQRGLAQSLLHDPKLLILDPTNGLDPAIGIREIRDYLRKLTR 180  
 Db 116 GLTGVGSKTKGFGSLGMRQRLGLAAALLGDEYILDEPYNGLDPEGLHWRVTLQNIAT 175  
 Qy 181 EKNMAVIVSSHLLSEMELMCDRIATIIQNGKL 211  
 Db 176 Q-GRTVLVSSHLLSEMAQTAHLIVIGRGKL 205

RESULT 15

US-09-252-991A-28171  
 ; Sequence 28171, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 28171  
 ; LENGTH: 788  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-28171

Query Match 24.7%; Score 381; DB 2; Length 788;  
 Best Local Similarity 31.8%; Pred. No. 4.9e-28;  
 Matches 97; Conservative 57; Mismatches 111; Indels 40; Gaps 6;  
 Qy 3 TLELKNVSKTIRGKIIIEGLSPDVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAGEIA 62  
 Db 486 SLVEIDGATLYRYGALTALSGDLRLLEPEGEVLGLGHNGAGKTTTIVLGLLAPSEGEVR 545  
 Qy 63 VCGSVKNEFEKAARHGAIVENPELYKFLTGYNLOQYARMKGVTKKKIDEIVELVGL 122  
 Db 546 VLGHDAARS--LEARRQLGYLPENVTFFPQLSGAETLRHFARL-KGVAPAEAAARLLEQVGL 602  
 Qy 123 KVRINDKVTYSIGMRQRGLAQSLLHDPKLLILDPTNGLDPAIGIREIRDYLRKLTR 182  
 Db 603 GHAAARRRLKTYSGMRQRGLAQSLLHDPKLLILDPTNGLDPAIGIREIRDYLRKLTR 661  
 Qy 183 GMAVIVSSHLLSEMELMCDRIATIIQNGKLRIQHVHGPARDKRYVYIQADDTQALTREA 242  
 Db 662 GTGIVLCSHVLPGVETHIDRAAILAGRLQ-----VAGSLAELRKA 703  
 Qy 243 AAFRKVKVDEAEGGIELSIQKQREVPDLIKHLTDSGVRVLYEVKAVNKSLEDRFLFEITADKE 302  
 Db 704 ALPTRVRLASPHN-----PQWLE-----RWHRAGLAARLLDDQRIEVLDDA 745  
 Qy 303 EAGHV 307  
 Db 746 ERDGV 750

Search completed: July 13, 2006, 13:50:40  
 Job time : 52 secs

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GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 13, 2006, 13:49:57 ; Search time 186 Seconds  
(without alignments)  
764.554 Million cell updates/sec

Title: US-10-510-941-2  
Perfect score: 1542  
Sequence: 1 LETLLEKNVSKTIRGKKII.....KSLDRFLEITADKEA QHV 307

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.psp:
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.psp:
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.psp:
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_PUBCOMB.psp:
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.psp:
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.psp:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1542	100.0	307	5	US-10-510-941-2
2	738.5	47.9	310	4	US-10-369-493-16618
3	734	47.6	301	4	US-10-282-122A-60404
4	734	47.6	301	6	US-11-045-004-182
5	639	41.4	306	6	US-11-045-004-885
6	638	41.4	309	5	US-10-510-386-84
7	536	34.8	302	4	US-10-282-122A-72352
8	535.5	34.7	306	4	US-10-369-493-17122
9	516	33.5	299	4	US-10-369-493-9838
10	493	32.0	306	4	US-10-369-493-20363
11	493	32.0	308	4	US-10-369-493-1297
12	491.5	31.9	318	4	US-10-369-493-1336
13	485	31.5	221	4	US-10-369-493-16570
14	473	30.7	305	4	US-10-369-493-21602
15	468	30.4	346	4	US-10-156-761-12401
16	455.5	29.5	306	4	US-10-282-122A-53430
17	447.5	29.0	287	4	US-10-282-122A-54022
18	447.5	29.0	377	5	US-10-501-282-5390
19	444	28.8	336	5	US-10-732-923-11559
20	438	28.4	311	4	US-10-369-493-11246
21	436	28.3	233	4	US-10-047-676A-12
22	436	28.3	233	5	US-10-790-914-12
23	435.5	28.2	237	4	US-10-369-493-18206
24	433.5	28.1	341	4	US-10-156-761-8470
25	432.5	28.0	310	4	US-10-282-122A-52344
26	431.5	28.0	305	4	US-10-369-493-18115
27	431.5	28.0	316	4	US-10-369-493-18754

28	431.5	28.0	339	5	US-10-732-923-1502	Sequence 1502, Ap
29	431.5	28.0	443	4	US-10-156-761-10399	Sequence 10399, A
30	431	28.0	308	4	US-10-156-761-14601	Sequence 14601, A
31	430.5	27.9	233	4	US-10-369-493-11165	Sequence 11165, A
32	429	27.8	312	3	US-09-738-626-6521	Sequence 6521, Ap
33	426.5	27.7	300	6	US-11-079-463-8196	Sequence 8196, Ap
34	425	27.6	308	4	US-10-369-493-16655	Sequence 16655, A
35	424.5	27.5	312	4	US-10-369-493-1202	Sequence 1202, Ap
36	424.5	27.5	316	4	US-10-369-493-20198	Sequence 20198, A
37	424.5	27.5	339	5	US-10-732-923-1771	Sequence 1771, Ap
38	422.5	27.4	310	5	US-10-732-923-1537	Sequence 1537, Ap
39	421.5	27.3	221	4	US-10-369-493-11149	Sequence 11149, A
40	421.5	27.3	310	4	US-10-369-493-17283	Sequence 17283, A
41	421	27.3	327	4	US-10-369-493-3029	Sequence 3029, Ap
42	420.5	27.3	248	5	US-10-474-792-392	Sequence 392, App
43	420.5	27.3	282	4	US-10-369-493-17469	Sequence 17469, A
44	420	27.2	312	4	US-10-369-493-1262	Sequence 1262, Ap
45	419	27.2	229	4	US-10-369-493-9672	Sequence 9672, Ap

ALIGNMENTS

RESULT 1  
US-10-510-941-2  
; Sequence 2, Application US/10510941  
; Publication NO. US20060040346A1  
; GENERAL INFORMATION:  
; APPLICANT: Jorgensen, Steen Troels  
; APPLICANT: Rasmussen, Michael Dolberg  
; APPLICANT: Andersen, Jens Tonne  
; APPLICANT: Olesen, Peter Bjarke  
; APPLICANT: Clausen, Ib Groth  
; TITLE OF INVENTION: Improved Bacillus Host Cell  
; FILE REFERENCE: 10297.204-US  
; CURRENT FILING DATE: 2004-10-08  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 2  
; TYPE: PRT  
; LENGTH: 307  
; ORGANISM: Bacillus licheniformis  
US-10-510-941-2

Query Match	100.0%;	Score 1542;	DB 5;	Length 307;
Best Local Similarity	100.0%;	Pred. No. 6.9e-123;		
Matches 307;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	LETLLEKNVSKTIRGKKII	EGLSFDVRAGEIFGFLGPN	GAGKTTTIRMIVGHMSITAGE 60
Db	1	LETLLEKNVSKTIRGKKII	EGLSFDVRAGEIFGFLGPN	GAGKTTTIRMIVGHMSITAGE 60
Qy	61	IACGVSVKENFEKAAHIGAI	VENPELYKFLGYNLQOQYAR	MTKGVTKKKIDIEIVELV 120
Db	61	IACGVSVKENFEKAAHIGAI	VENPELYKFLGYNLQOQYAR	MTKGVTKKKIDIEIVELV 120
Qy	121	GLKNRNDKVTYSLGMRQRLG	LAQSLHDPKLLIDEPNGLD	PAGIREIRYLRKLTR 180
Db	121	GLKNRNDKVTYSLGMRQRLG	LAQSLHDPKLLIDEPNGLD	PAGIREIRYLRKLTR 180
Qy	181	EKGMAVTVSHLLSELMCDRI	AIQNGKLRDIOHVHGPAREK	KYVYIQADDTQALTR 240
Db	181	EKGMAVTVSHLLSELMCDRI	AIQNGKLRDIOHVHGPAREK	KYVYIQADDTQALTR 240
Qy	241	EAAPFRKVKVDEAGGIELSI	QKDEVPDLIKHLTDSGRL	YEVKAVNKSLDRFLEITAD 300
Db	241	EAAPFRKVKVDEAGGIELSI	QKDEVPDLIKHLTDSGRL	YEVKAVNKSLDRFLEITAD 300
Qy	301	KEEAQHV 307		
Db	301	KEEAQHV 307		

```

RESULT 2
US-10-369-493-16618
; Sequence 16618, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 16618
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-10-369-493-16618

Query Match 47.9%; Score 738.5; DB 4; Length 310;
Best Local Similarity 48.5%; Pred. No. 2.1e-54;
Matches 147; Conservative 66; Mismatches 81; Indels 9; Gaps 3;

QY 1 LETLLEKNVKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAGE 60
D 10 MTTILSVRLDKVIGKKTLENISFDVKQGEVFGFLGPNAGKTTTIRMIVGLIKATEGT 69
QY 61 IAVCGSVKFNFEKARHICAIVENPELYKFLTGYNLOQYARMTKGVTKKKIDEIVELV 120
D 70 ISIGGSIKENFEARQIGSIVENPELYTLTGWENLKQFARMGLGDISDERIIEIAEW 129
QY 121 GLKNRNDKVTYSLGNRQRLGLAQSLHDPKLLILDEPTNGLDPAIGREIRDYRLKLT 180
D 130 HLDERHDKVTYSLGNKQRLGLAQALLGNPKLLILDEPTNGLDPAIGREIRDYRLK 189
QY 181 EKMAMIVSSHLLSEMELMCDRIAIIQNGKL---RDIOHVHGPARDKKRYIIQADDTQA 237
D 190 EENSVFISHLSEVQMICDRVAIIHKGMITVAKVEELIKTASDRVEMIVTPISKAKD 249
QY 238 LTRAAAFKRYKDEAEGGELSIOKD--EVPDLIKHLTDSGVRLYEVKAVNKSLEDF 295
D 250 MLEAAKEVREVSVE---GRLICRMDIASISSWNKHFVENEIDVHVSXVELVFTLED 305
QY 296 EIT 298
D 306 ELT 308

RESULT 3
US-10-282-122A-60404
; Sequence 60404, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.0344

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; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60404
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
US-10-282-122A-60404

Query Match 47.6%; Score 734; DB 4; Length 301;
Best Local Similarity 49.8%; Pred. No. 4.8e-54;
Matches 149; Conservative 61; Mismatches 81; Indels 8; Gaps 3;

QY 2 ETLELKNVKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAGEI 61
D 3 ERALQVNTNLRKIRKEIIKIGISFEVMPGEVFGFLGPNAGKTTTIRMIVGLIKPTSGTI 62
QY 62 AVCGVSVKFNFEKARHICAIVENPELYKFLTGYNLOQYARMTKGVTKKKIDEIVELV 121
D 63 LGGKDIRKNFTFAMRGLSIVENPEFYFLTGQENLAYFARMDSIKKERIQEVTELVG 122
QY 122 LKNRNDKVTYSLGNRQRLGLAQSLHDPKLLILDEPTNGLDPAIGREIRDYRLKLTRE 181
D 123 LEKRNDRVSTYSLGNRQRLGLAQALLSNPKLLILDEPTNGLDPSGIHMRDPIRALARN 182
QY 182 KGMAMIVSSHLLSEMELMCDRIAIIQNGK-LRDIQHVHGPARDKKRYIIQADDTQALTR 240
D 183 EGISVLVSSHLLSEIELLCCDRVAIMTDGTIIKTDQVAHLLSSRAQLRWVTP-----IE 236
QY 241 EAAAF-RKVKVDEAEGGELSIOKQVDPDLIKHLTDSGVRLYEVKAVNKSLEDFLEIT 298
D 237 QAKAFLESVTEVDEGEYLVVTANNEESAENWOLVAKGIKVHEIDKKRPSLEDFLEIT 295

RESULT 4
US-11-045-004-182
; Sequence 182, Application US/11045004
; Publication No. US20060078901A1
; GENERAL INFORMATION:
; APPLICANT: BUCHRIESEN, CARMEN
; APPLICANT: FRANGEUL, LIONEL
; APPLICANT: COUVE, ELISABETH
; APPLICANT: RUSNIOK, CHRISTOPHE
; APPLICANT: FSIHI, HAFIDA
; APPLICANT: DEHOUX, PIERRE
; APPLICANT: DUSSURGET, OLIVIER
; APPLICANT: CHETOUANI, FARID
; APPLICANT: NEDJARI, HAFED
; APPLICANT: GLASER, PHILIPPE
; APPLICANT: KUNST, FRANCK
; APPLICANT: COSSART, PASCALE

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; APPLICANT: DANIELS, JUSTIN
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KREFT, JURGEN
; APPLICANT: KUHN, MICHAEL
; APPLICANT: NG, EVA
; APPLICANT: VAZQUEZ-BOLAND, ANTONIO
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
; APPLICANT: GARRIDO-GARCIA, PATRICIA
; APPLICANT: TIERREZ-MARTINEZ, ALBERTO
; APPLICANT: AMEND, ALEXANDRA
; APPLICANT: CHAKRABORTY, TRINAD
; APPLICANT: DOMANN, EUGEN
; APPLICANT: HAIN, THORSTEN
; APPLICANT: BERCHÉ, PATRICK
; APPLICANT: CHARBIT, ALAIN
; APPLICANT: DURANT, LIONEL
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
; APPLICANT: BAQUERO, FERNANDO
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
; APPLICANT: GOMEZ-LOPEZ, NURIA
; APPLICANT: MADUENIO, ENCARN
; APPLICANT: PABLOS, BETRIZ DE
; APPLICANT: WEHLAND, JURGEN
; APPLICANT: KARST, UWE
; APPLICANT: ENTIAN, KARL-DIETER
; APPLICANT: HAUF, JORG
; APPLICANT: ROSE, MATTHIAS
; APPLICANT: VOSS, HAMUT
; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
; FILE REFERENCE: 05394.0018-02
; CURRENT APPLICATION NUMBER: US/11/045,004
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/637,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: 10/257,023
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: PCT/FR01/01118
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: FR 00/04,629
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2854
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 182
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
; US-11-045-004-182

Query Match 47.6%; Score 734; DB 6; Length 301;
Best Local Similarity 49.8%; Pred. No. 4.8e-54;
Matches 149; Conservative 61; Mismatches 81; Indels 8; Gaps 3;

QY 2 ETLELKNVSKTIRGKKIIEGLSFDVRAGEIFGLGPNAGAGKTTTIRMIVGHMSITAGEI 61
DB 3 ERALQVTLNKKIRKEIKIGISFEVMPGEVFGFLGPNAGAGKTTTIRMIVGLIKPTSGTI 62

QY 62 AVCGSVKNEFKAARHGAIVENPELYKELTYQNLQOYARMTKGVTKKKIDEIVELVG 121
DB 63 LIGGKDIRKFTMEAGLSIVENPEFYFTLTQENLAYFARMSSIKKRIQEVTELVG 122

QY 122 LKGRINDKVTYSLGNRQLGSAQLLHPKLLILDEPTNGLDIPAGIREIDYRLKLTRE 181
DB 123 LKGRINDRVTYSLGNRQLGSAQLLHPKLLILDEPTNGLDIPAGIREIDYRLKLTRE 182

QY 182 KGNMVTSSHLISEMLCMCDRIAIIQNGK-LRDIQHVHGPARDKRYKRYIQADDTQALTR 240
DB 183 EGISVLVSSHLLSEIELLCCORVAIMTDGTTIKTDQVAHLLSSRAQLRWVTP-----IS 236

QY 241 EAAAP-RKKVDPAEGGIELSTOKDEVPDLIKHLTDSGVRVLYEVKAVNKSLDRFLEIT 298
DB 237 QAKAFLESYTEVDGEYLVVTAMNEESAENQOLVAKGIKVHEIDKRRKPSLEDLFLELT 295

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RESULT 5
US-11-045-004-885
; Sequence 885, Application US/11045004
; Publication No. US20060078901A1
; GENERAL INFORMATION:
; APPLICANT: BUCHRIEGER, CARMEN
; APPLICANT: FRANGEUL, LIONEL
; APPLICANT: COUVE, ELISABETH
; APPLICANT: RUSNIOK, CHRISTOPHE
; APPLICANT: FSIHL, HAFIDA
; APPLICANT: DEHOUX, PIERRE
; APPLICANT: DUSSURGET, OLIVIER
; APPLICANT: CHETOUANI, FARID
; APPLICANT: NEDJARI, HAFED
; APPLICANT: GLASER, PHILIPPE
; APPLICANT: KUNST, FRANK
; APPLICANT: COSSART, PASCALE
; APPLICANT: DANIELS, JUSTIN
; APPLICANT: GOEBEL, WERNER
; APPLICANT: KREFT, JURGEN
; APPLICANT: KUHN, MICHAEL
; APPLICANT: NG, EVA
; APPLICANT: VAZQUEZ-BOLAND, ANTONIO
; APPLICANT: DOMINGUEZ-BERNAL, GUSTAVO
; APPLICANT: GARRIDO-GARCIA, PATRICIA
; APPLICANT: TIERREZ-MARTINEZ, ALBERTO
; APPLICANT: AMEND, ALEXANDRA
; APPLICANT: CHAKRABORTY, TRINAD
; APPLICANT: DOMANN, EUGEN
; APPLICANT: HAIN, THORSTEN
; APPLICANT: BERCHÉ, PATRICK
; APPLICANT: CHARBIT, ALAIN
; APPLICANT: DURANT, LIONEL
; APPLICANT: PEREZ-DIAZ, JOSE-CLAUDIO
; APPLICANT: BAQUERO, FERNANDO
; APPLICANT: GARCIA DEL PORTILLO, FRANCISCO
; APPLICANT: GOMEZ-LOPEZ, NURIA
; APPLICANT: MADUENIO, ENCARN
; APPLICANT: PABLOS, BETRIZ DE
; APPLICANT: WEHLAND, JURGEN
; APPLICANT: KARST, UWE
; APPLICANT: ENTIAN, KARL-DIETER
; APPLICANT: HAUF, JORG
; APPLICANT: ROSE, MATTHIAS
; APPLICANT: VOSS, HAMUT
; TITLE OF INVENTION: LISTERIA MONOCYTOGENES GENOME, POLYPEPTIDES AND USES
; FILE REFERENCE: 05394.0018-02
; CURRENT APPLICATION NUMBER: US/11/045,004
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: 10/637,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: 10/257,023
; PRIOR FILING DATE: 2002-10-08
; PRIOR APPLICATION NUMBER: PCT/FR01/01118
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: FR 00/04,629
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 2854
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 885
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Listeria monocytogenes
; US-11-045-004-885

Query Match 41.4%; Score 639; DB 6; Length 306;
Best Local Similarity 45.3%; Pred. No. 6.1e-46;
Matches 135; Conservative 57; Mismatches 104; Indels 2; Gaps 2;

QY 2 ETLELKNVSKTIRGKKIIEGLSFDVRAGEIFGLGPNAGAGKTTTIRMIVGHMSITAGEI 61
DB 3 ETVLKLHVTKKIGQKNIIVHDSFDIHKGEVFGLLGPNAGAGKTTTIRSIIVGLIRSEGTV 62

```







; Sequence 1297, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 1297  
; LENGTH: 308  
; TYPE: PRT  
; ORGANISM: Pyrococcus horikoshii  
US-10-369-493-1297

Query Match 32.0%; Score 493; DB 4; Length 308;  
Best Local Similarity 36.4%; Pred. No. 1.7e-33;  
Matches 118; Conservative 67; Mismatches 91; Indels 48; Gaps 7;  
QY 5 LELKNVSKTIRGKIIIEGLSFDVRAGEIFGFLGPNAGAGKTTTIRMIVGHMSITAGIACV 64  
DB 4 IEVEKUTSKYGFKAIDNLSFVVDGIVGFLGPNAGAGKTTTILSMGLIIPDSGDVRL 63  
QY 65 GVSVKENFEKAARHIGAIIVENPELYKFLTYGQNLQOYA---RMTKGVTKKKIDIEIVELVG 121  
DB 64 GYDIPKEPLKAKERLGLPENAIYEELTAWNLDFPASFYRMSKQEKRIEELKLVG 123  
QY 122 LKNRINDKVTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAIGREIRYLRKLTRE 181  
DB 124 LWDVRYKAKTFSGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAIGREIRYLRKLTRE 182  
QY 182 KGMNAVIVSSHLLSEMELMCDRIAIIONGKLRDIQHVHGPARDKRYIQAADTQALTR 241  
DB 183 OGKTVFSSHLLSEVELADKGVIIYVKGKLRV---GTLEEIKQY-----ME 227  
QY 242 AAARFKVKVDEAGGIELSQKDEVPDLIK-----HLTDSGV 278  
DB 228 LEGY-BIKIETKQPLPEL-----EIPDIIRIETKTENKAIIFAKSDIRESISELAKGI 281  
QY 279 RLYEVKAVNKSLEDRFLEITADKE 302  
DB 282 TIISLEIEPSELDVFLKTYRRE 305

RESULT 12  
US-10-369-493-1336  
; Sequence 1336, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 1336  
; LENGTH: 318  
; TYPE: PRT  
; ORGANISM: Pyrococcus horikoshii

US-10-369-493-1336

Query Match 31.9%; Score 491.5; DB 4; Length 318;  
Best Local Similarity 35.2%; Pred. No. 2.4e-33;  
Matches 112; Conservative 78; Mismatches 97; Indels 31; Gaps 7;  
QY 4 LLELKNVSKTIRGKII-----IEGLSFDVRAGEIFGFLGPNAGAGKTTTIRMIV 51  
DB 3 VIEVNLNRK-LYPKKIPLPFRKVFWEALGKITFRVKGELFGLGPNAGAGKTTTILKILT 61  
QY 52 GHMSITAGEIAVCGVSVKENFEKAARHIGAIIVENPE-LYKFLTYGQNLQOYAR---MTKG 107  
DB 62 TLLEPSSGSEAKVLGDLVDVKDAREIKRINLVAEGERTLYRWLTAIYENLRYFASIIYIPRR 121  
QY 108 VTKKKIDIEIVELVGLKNRINDKVTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPA 167  
DB 122 EAEKRIEELLKNVGLWDRNDLVNYSRGMKQRLAKALINDPEVLFLDEPTGLDQVS 181  
QY 168 IREIRDYLRKLTREKGMNAVIVSSHLLSEMELMCDRIAIIONGKLRDIQHVHGPARDK 227  
DB 182 AVFVRELVRRLVDEEGKTVLLTTHVMNEAEELCDRIAIIDHGKIIAALNTPEGLKR----- 236  
QY 228 YVIQADDTQALTR-----EAAAFRKVKVDEAGGIEL--SIOKDEVPDLIKHLTDSG 280  
DB 237 --WVRNDTIVFVRNYPGVNPFGLVKVDNRGVILRGLSLEEEIPKLVFLVKSNAKV 294  
QY 281 YEVKAVNKSLEDRFLEIT 298  
DB 295 LSVEVKEPTLEDVFIKLT 312

RESULT 13  
US-10-369-493-16570  
; Sequence 16570, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianfeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 16570  
; LENGTH: 221  
; TYPE: PRT  
; ORGANISM: Bacillus thuringiensis  
US-10-369-493-16570

Query Match 31.5%; Score 485; DB 4; Length 221;  
Best Local Similarity 46.2%; Pred. No. 5.2e-33;  
Matches 98; Conservative 51; Mismatches 61; Indels 2; Gaps 2;  
QY 1 LETLLEKNVSKTIRGKIIIEGLSFDVRAGEIFGFLGPNAGAGKTTTIRMIVGHMSITAGE 60  
DB 1 INTIHTKTLTKVYGKSDVNLININVOQGEIYVGFGRNGAGKTTTIRMILLSLIKPSTSGT 60  
QY 61 IAVCGVSVKENFEKAARHIGAIIVENPELYKFLTYGQNLQOYARMTKGVTKK-IDEIVEL 119  
DB 61 IEIFGENLFQNKQDILSRIGSIIVEVGFENLTAKENLLINAKII-GVHKNAIEEALEI 119  
QY 120 VGLKNRINDKVTYSLGMRQRLGLAQSLLHDPKLLILDEPTNGLDPAIGREIRDYLRKLT 179  
DB 120 VGLQHETKVLGVGYSLGMRQRLGIARALLHYPELLILDEPTNGLDPTGIGEMRKLHLSLA 179  
QY 180 REKGMNAVIVSSHLLSEMELMCDRIAIIONGKL 211

Db 180 QERNITLISSHILAEIEQLVDRIIGIIEGKL 211

## RESULT 14

US-10-369-493-21602  
; Sequence 21602, Application US/10369493  
; Publication No. US20030233675A1

## ; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 21602

; LENGTH: 305

; TYPE: PRT

; ORGANISM: Pyrococcus abyssi

US-10-369-493-21602

Query Match 30.7%; Score 473; DB 4; Length 305;

Best Local Similarity 35.3%; Pred. No. 8.5e-32;

Matches 107; Conservative 77; Mismatches 103; Indels 16; Gaps 4;

Qy 4 LLELKNVKTIRGKIIIEGLSFVRAGEIFGFLGPNAGAKTTTIRMIVGHMSITAGEIAV 63

Db 3 VIEIENUTKYGKFKAVDNLSLEVEKIIIFGFLGPNAGAKTTTILSLMGLIIPDSGSRVL 62

Qy 64 CGSVKENFEKAARHIGAIVENPELYKFLTYQNLOQYA---RMTKGVTKKKIDIEIVELY 120

Db 63 LGYDIFKEPIKAKERLGFLENATIEELTAWRNLDFFASFYNIPKQEKKEKRIEELKLV 122

Qy 121 GLKNRINDKVTYSLGNRQLGIAQSLHDPKLLILDEPTNGLDPPAGIREIRYLRKLT 180

Db 123 GLWDVRYRKVKSFGKMKORLLAQAALINDPELLILDEPTSGLDPPQCARLVKQIILE-QK 181

Qy 181 EKMNAVIVSHLLSEMELMCDRIALIQNGKLRDIOHVHGPARDKKRYIIQADDTQALTR 240

Db 182 KQSKTFFFSHILSEVELADKVGIIIVKGLRTVGTU-----EIKKQYNELEGYEIKVE 236

Qy 241 EAAAFKRVKVDY-----AEGGIELSIOKDEVPDLIKHLTDSGVRLYEYKAVNKSLEDR 293

Db 237 TKQFPPEIPLDVIRIEKIADNKVLIIPAKSDIREILSEELSKRGITVLSLEIEPSLEDV 296

Qy 294 FLE 296

Db 297 FLK 299

## RESULT 15

US-10-156-761-12401

; Sequence 12401, Application US/10156761

; Publication No. US20030119018A1

## ; GENERAL INFORMATION:

; APPLICANT: OMURA, SATOSHI

; APPLICANT: IKEDA, HARUO

; APPLICANT: ISHIKAWA, JUN

; APPLICANT: HORIKAWA, HIROSHI

; APPLICANT: SHIBA, TADAYOSHI

; APPLICANT: SAKAKI, YOSHIYUKI

; APPLICANT: HATTORI, MASAHIRA

; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

; FILE REFERENCE: 249-262

; CURRENT APPLICATION NUMBER: US/10/156,761

; CURRENT FILING DATE: 2002-05-29

; PRIOR APPLICATION NUMBER: JP 2001-204089

; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697

; PRIOR FILING DATE: 2001-08-02

; NUMBER OF SEQ ID NOS: 15109

; SEQ ID NO 12401

; LENGTH: 346

; TYPE: PRT

; ORGANISM: Streptomyces avermitilis

US-10-156-761-12401

Query Match 30.4%; Score 468; DB 4; Length 346;

Best Local Similarity 37.0%; Pred. No. 2.7e-31;

Matches 113; Conservative 54; Mismatches 114; Indels 24; Gaps 6;

Qy 10 VSKTIRGKKI-IEGLSPDVRAGEIFGFLGPNAGAKTTTIRMIVGHMSITAGEIAVCGYSV 68

Db 46 LTKRYRGQLAVDGLDLTVPAGSVFGFLGPNAGAKTTTIRMIVGHMSITAGEIAVCGYSV 105

Qy 69 KENPEKAARHIGAIVENPELYKFLTYQNLOQY---ARMTKGVTKKKIDIEIVELVGLKN 124

Db 106 PRSARTVLPHGALIEGPAIYGFSLGRDNLRLRYDAADPTADPTRTTFRVAATLDRVGLTA 165

Qy 125 RINDKVTYSLGNRQLGIAQSLHDPKLLILDEPTNGLDPPAGIREIRYLRKLTREKGM 184

Db 166 AAGKKAKAYSILGKMKRLGAAALIQPRLLVLDDEPTNGLDPPQGMREIRSLVRELASD-GT 224

Qy 185 AVIVSSHLLSEMELMCDRIALIQNGKLRDIOHVHGPARDKKRYIIQADDTQALTREAAA 244

Db 225 TVFLSSHLLDEIEBQVCTHAAVMAQGRLLITQGAVALAAGARGRLVVTTPD-----VTDA- 279

Qy 245 FRKVKVDEAEGGIELSIOKD-----EVPDLIKHLTDSGVRLYEYKAVNKSLEDRFL 295

Db 280 ----RVLKEQGVADIIVAEEDRVVTGEPDPPDGLAELNAALVTAARVVRGFGVERASLEDAFV 335

Qy 296 EITAD 300

Db 336 ALTGE 340

Search completed: July 13, 2006, 13:53:52

Job time : 187 secs

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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2006, 13:50:52 ; Search time 29 Seconds  
(without alignments)  
605.617 Million cell updates/sec

Title: US-10-510-941-2  
Perfect score: 1542  
Sequence: 1 LETLLEKNVSKTIRGKKII.....KSLDRFLFETADKERAQHV 307

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 204771 seqs, 57208143 residues

Total number of hits satisfying chosen parameters: 204771

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New\*

- 1: /EMC Celerra\_SID33/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 2: /EMC Celerra\_SID33/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 3: /EMC Celerra\_SID33/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /EMC Celerra\_SID33/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 5: /EMC Celerra\_SID33/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 6: /EMC Celerra\_SID33/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 7: /EMC Celerra\_SID33/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /EMC Celerra\_SID33/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	411.5	26.7	231	6	US-10-471-571A-3584
2	404.5	26.2	230	6	US-10-471-571A-1354
3	392.5	25.5	232	6	US-10-471-571A-716
4	349.5	22.7	558	7	US-11-293-697-4274
5	346.5	22.5	1704	7	US-11-289-102-341
6	338	21.9	299	6	US-10-471-571A-4370
7	331.5	21.5	949	6	US-10-449-902-43324
8	331.5	21.5	949	6	US-10-449-902-44592
9	316.5	20.5	304	7	US-11-274-683-30
10	315.5	20.5	968	6	US-10-449-902-54801
11	314	20.4	815	7	US-11-293-697-4238
12	303.5	19.7	559	7	US-11-293-697-2603
13	301.5	19.6	325	6	US-10-471-571A-3086
14	296.5	19.2	341	6	US-10-471-571A-2868
15	294	19.1	236	6	US-10-471-571A-1718
16	292.5	19.0	342	6	US-10-471-571A-1718
17	292	18.9	313	6	US-10-471-571A-4896
18	287.5	18.6	199	7	US-11-133-075-62
19	275.5	17.9	423	6	US-10-471-571A-5286
20	274	17.8	355	6	US-10-471-571A-2570
21	272	17.6	302	6	US-10-471-571A-1646
22	267.5	17.3	353	6	US-10-449-902-49749
23	262.5	17.0	261	6	US-10-471-571A-496
24	254.5	16.5	282	6	US-10-471-571A-1908
25	253	16.4	364	6	US-10-471-571A-5014

26	249.5	16.2	243	6	US-10-471-571A-5186
27	249.5	16.2	692	7	US-11-056-355B-45974
28	249.5	16.1	298	6	US-10-471-571A-1350
29	248.5	16.1	678	7	US-11-056-355B-79452
30	245	15.9	291	6	US-10-449-902-35418
31	245	15.9	346	6	US-10-449-902-40549
32	243	15.8	219	6	US-10-471-571A-2420
33	243	15.8	253	6	US-10-471-571A-3050
34	242	15.7	651	6	US-10-471-571A-252
35	240.5	15.6	260	6	US-10-471-571A-2740
36	238	15.4	262	7	US-11-174-307B-3916
37	237	15.4	263	6	US-10-953-349-6892
38	234.5	15.2	1187	7	US-11-056-355B-73529
39	234.5	15.2	1216	7	US-11-056-355B-73528
40	234.5	15.2	1227	7	US-11-056-355B-73527
41	234.5	15.2	1258	7	US-11-056-355B-85264
42	234.5	15.2	1287	7	US-11-056-355B-85263
43	234.5	15.2	1298	7	US-11-056-355B-85262
44	233	15.1	1199	7	US-11-056-355B-83585
45	233	15.1	1213	7	US-11-056-355B-83584

## ALIGNMENTS

### RESULT 1

US-10-471-571A-3584  
; Sequence 3584, Application US/10471571A  
; Publication No. US20060115490A1  
; GENERAL INFORMATION:

; APPLICANT: CHIRON SPA  
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE: P026227WO  
; CURRENT APPLICATION NUMBER: US/10/471,571A  
; CURRENT FILING DATE: 2003-09-12  
; PRIOR APPLICATION NUMBER: GB-0107661.1  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 5642  
; SOFTWARE: Seqwin99, version 1.03  
; SEQ ID NO 3584  
; LENGTH: 231  
; TYPE: PRT

; ORGANISM: Staphylococcus aureus  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(231)  
; OTHER INFORMATION: hypothetical protein  
US-10-471-571A-3584

Query Match 26.7%; Score 411.5; DB 6; Length 231;  
Best Local Similarity 37.3%; Pred. No. 1.5e-21;  
Matches 84; Conservative 61; Mismatches 65; Indels 15; Gaps 4;

Qy	4	LLELNKVS	KTI	R	G	K	K	I	I	E	G	L	S	F	D	V	R	A	G	E	I	F	G	F	L	G	P	N	A	G	K	T	T	T	I	R	M	I	V	G	H	M	S	I	T	A	G	E	T	A	V	63																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																													
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Qy	124	N	R	I	N	D	K	V	K	T	Y	S	L	G	M	R	Q	L	G	A	L	Q	S	L	H	D	P	K	L	I	L	D	E	P	T	N	G	L	D	P	A	G	I	R	E	I	R	D	Y	L	R	K	L	T	R	E	K	G	183																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
Db	114	E	Y	H	K	K	A	K	T	Y	S	L	G	M	R	K	Q	I	G	I	A	I	A	F	L	N	K	P	Q	F	I	L	D	E	P	N	G	L	D	P	K	A	V	R	D	R	E	L	I	V	Q	A	O	E	-	G	172																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																								
Qy	184	M	A	V	I	V	S	H	L	L	S	E	M	L	M	C	D	R	I	A	I	I	Q	N	G	K	L	R	D	I	Q	H	V	G	H	G	P	A	R	D	E	K	R	Y	228																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
Db	173	V	T	F	L	S	S	H	I	L	S	E	L	V	K	I	T	S	I	L	I	N	K	G	K	I	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

### RESULT 2

US-10-471-571A-1354  
; Sequence 1354, Application US/10471571A

```

; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 1354
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(290)
; OTHER INFORMATION: hypothetical protein
US-10-471-571A-1354

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Query Match      26.2%; Score 404.5; DB 6; Length 290;
Best Local Similarity 31.2%; Pred. No. 6e-21;
Matches 94; Conservative 76; Mismatches 106; Indels 25; Gaps 8;

QY 5 LELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGAGKTTTIRMIVGHMSITAGIAVC 64
bb 1 MKLEHITKKYGSNVVNDIDFDGDSRIIVGLIGNGVGKTTVMKVMNGNIIRFDGKVDI- 59
QY 65 GVSVKENFEKAARHIGAIVENPELYKFLTYGQNLQOYAR-MTKGVTKKKIDEIVELVGLK 123
Db 60 -----DN-----ADNIGFLIEHPKLYDNKSGLYNLKLFQAVLGKGFDAVTDKIIDAFGMR 110
QY 124 NRINDKVTYSLGMRQRLGALSHLHDPKLLIILDEPTNGLDPAIGIREIDYLRKLTREK 183
Db 111 PYIKKKVKYKSMGKQKLAIVSLMKNPKPLIILDEPTNGMDPDGSDIVLTITKSLVNELD 170
QY 184 MAVIVSHLLSEMELMCDRIAIONGK-LRDIQHVHGPARD-----EKRYVIOADDTQ 236
Db 171 MRILSHKLEDIELICDRAVFRDGHFQVDVNMEEGVASDTTIVTDHKDF-----DRTE 226
QY 237 ALTREAAAFKRVKVDAAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVKAVNKSLEDRFLE 296
Db 227 KYLAE--HFQLQNVDRADGHLMINAQKN-YQVILKALSELDIYPKVIETRKSSLRDTYFN 283
QY 297 I 297
Db 284 I 284

```

```

RESULT 3
US-10-471-571A-716
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927WO
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 716
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(232)
; OTHER INFORMATION: hypothetical protein
US-10-471-571A-716

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```

Query Match      25.5%; Score 392.5; DB 6; Length 232;
Best Local Similarity 38.0%; Pred. No. 3e-20;
Matches 79; Conservative 55; Mismatches 69; Indels 5; Gaps 3;

QY 5 LELKNVSKTIRGKKIIEGLSFDVRAGEIFGFLGPNAGAGKTTTIRMIVGHMSITAGIAVC 64
Db 6 LVTENISKRFKNQDVLKHINITLENNEVYGLGINGAGKTTLMKIIICGILQODSGSIKLD 65
QY 65 GVSVKENFEKAARHIGAIVENPELYKFLTYGQNLQOYARMTKGVTKKKIDEIVELVGLKN 124
Db 66 NRPMTN-----DLHKVGLSIIETATYVHLSAQDNL-KIVCLNESVDSEINSLVSLNINV 121
QY 125 RINDKVTYSLGMRQRLGALSHLHDPKLLIILDEPTNGLDPAIGIREIDYLRKLTREKGM 184
Db 122 DKKKKVKDFSLGMKQRLGALAMALIKKPEILVLDEPSNGLDPIYQIELRELLKLT-EOGT 180
QY 185 AVIVSHLLSEMELMCDRIAIONGKLR 212
Db 181 SIIISSHILSEIQVLADHIGIIEHGEELK 208

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RESULT 4
US-11-293-697-4274
; Sequence 4274, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4274
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4274

Query Match      22.7%; Score 349.5; DB 7; Length 558;
Best Local Similarity 30.2%; Pred. No. 9e-17;
Matches 101; Conservative 68; Mismatches 108; Indels 57; Gaps 13;

QY 4 LLELKNVSKTIRGKKI--IEGLSFDVRAGEIFGFLGPNAGAGKTTTIRMIVGHMSITAGEI 61
Db 204 VLVLRLNLTKYRGQRMPAVDRCLGIPPGCECFLLGVNGAGKTTSTFRVVTGDTLASRGEA 263
QY 62 AVCGSVSVKENFEKAARHI--GAIVENPELYKFLTYGQNLQOYARMTKGVTKKKIDEI--- 116
Db 264 VLAGHSVAR--EPSAAHLSMGYCPQSDAIFELTGREHLELLARL-RGVPEAQVAQTGS 320
QY 117 -VELVGLKNRINDKVTYSLGMRQRLGALSHLHDPKLLIILDEPTNGLDPAIGIREIDYL 175
Db 321 GLARGLSLYADRPAGTYSGGNKRKLATALAVDPAVFLDDEPTTGMDPSARRFLNLSL 380
QY 176 RKLTRKGMMAVIVSHLLSEMELMCDRIAIONGKLRDI---QHVHG----- 219
Db 381 LAVVRE-GRSVMLTSHMEECEALCSRLAIWNGRFRCLGSPQHLKGRFAAGHTLTURVP 439
QY 220 PARDEKKRYIOADDTQALTRAAAFKRVKVDAAEGGIELSIQKDEVP----- 267
Db 440 AARSQPAAPAV-----AAEFPGAELREAHGG-RLRFQ---LPPGGRCALARVFG 484
QY 268 DLIKHLTDSGVRLYEVKAVNKSLEDRFLEITADK 301
Db 485 ELAVHGAHGEHVEDFSVS--QTMLEEVFLYFSKQD 516

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RESULT 5
US-11-289-102-341

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Db 810 QAKRDR--AIVLTTHSMEAEVLCRLCINVDGSLQCI---GTPKELIARYGGYYVLTM 863  
 QY 233 -----DDTQALTREAAA-FRKVKYDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVK 284  
 Db 864 TTSPEPEQEVENLARKSPNARKYVHLSGTQKVELPKQVRIADVPM-AVENFKRRTTEVQ 922  
 QY 285 A---VNKSLEDFLEITADKEEAQHV 307  
 Db 923 AWGLADTTMEDVFKVAKGQSSEEL 948

RESULT 8  
 US-10-449-902-44592  
 ; Sequence 44592, Application US/10449902  
 ; Publication No. US20060123505A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: National Institute of Agrobiological Sciences.  
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
 ; APPLICANT: The Institute of Physical and Chemical Research.  
 ; APPLICANT: Foundation for Advancement of International Science.  
 ; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
 ; FILE REFERENCE: MOA-A0205Y1-US  
 ; CURRENT APPLICATION NUMBER: US/10/449,902  
 ; CURRENT FILING DATE: 2003-05-29  
 ; PRIOR APPLICATION NUMBER: JP 2002-203269  
 ; PRIOR FILING DATE: 2002-05-30  
 ; PRIOR APPLICATION NUMBER: JP 2002-383870  
 ; PRIOR FILING DATE: 2002-12-11  
 ; NUMBER OF SEQ ID NOS: 56791  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 44592  
 ; LENGTH: 949  
 ; TYPE: PRT  
 ; ORGANISM: Oryza sativa  
 ; ORGANISM: Oryza sativa  
 US-10-449-902-44592

Query Match 21.5%; Score 331.5; DB 6; Length 949;  
 Best Local Similarity 29.4%; Pred. No. 3.2e-15;  
 Matches 96; Conservative 75; Mismatches 120; Indels 35; Gaps 12;  
 QY 9 NVSKTRGKK-----IIIEGLSPDVRAIGFPGFGLGNGAGKTTTIRMIVGHMSITAGEIA 62  
 Db 631 DLKKVYHGKGNPKDFAVRGLSLALPYGECGLTGLGNGAGKSFISMIGLTRPTSGNAF 690  
 QY 63 VCGSVKENPEKAARHIGAVENPELYKFLTGYNLQOQYARMTKGVTKKKIDIV-ELVG 121  
 Db 691 VREFSIQTMEKYNKNGVCPQNDMLWMLTGREHLOFYGRL-KSLNGSDLDTAVNESLR 749  
 QY 122 LKNRIN---DK-VKTYSLGMRQRLGLAOSLLHDPKLLILDEPTNGLDPAGIREIRDYLR 176  
 Db 750 SVNLLHGGAPDKQVKYSGMKRRLSVAISLIGDAKVVMYDEPSTGLDPASRKSILDAVK 809  
 QY 177 KLTREGMAVIVSSHLLSEMELMCDRIATIQNGKLRDIQHVGPARDKKR---YIIQA- 232  
 Db 810 QAKRDR--AIVLTTHSMEAEVLCRLCINVDGSLQCI---GTPKELIARYGGYYVLTM 863  
 QY 233 -----DDTQALTREAAA-FRKVKYDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYEVK 284  
 Db 864 TTSPEPEQEVENLARKSPNARKYVHLSGTQKVELPKQVRIADVPM-AVENFKRRTTEVQ 922  
 QY 285 A---VNKSLEDFLEITADKEEAQHV 307  
 Db 923 AWGLADTTMEDVFKVAKGQSSEEL 948

RESULT 9  
 US-11-274-683-30  
 ; Sequence 30, Application US/11274683  
 ; Publication No. US20060141583A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wyeth  
 ; APPLICANT: Haitli, Bradley A  
 ; TITLE OF INVENTION: Elaiophyllin biosynthetic gene cluster

FILE REFERENCE: 1855/256  
 ; CURRENT APPLICATION NUMBER: US/11/274,683  
 ; CURRENT FILING DATE: 2005-11-14  
 ; PRIOR APPLICATION NUMBER: US 60/627,752  
 ; PRIOR FILING DATE: 2004-11-12  
 ; NUMBER OF SEQ ID NOS: 55  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 30  
 ; LENGTH: 304  
 ; TYPE: PRT  
 ; ORGANISM: Streptomyces sp. NRRL 30748  
 ; ORGANISM: Streptomyces sp. NRRL 30748  
 US-11-274-683-30  
 Query Match 20.5%; Score 316.5; DB 7; Length 304;  
 Best Local Similarity 27.9%; Pred. No. 7.8e-15;  
 Matches 89; Conservative 64; Mismatches 125; Indels 41; Gaps 8;  
 QY 4 LLELKNVSKTRGKKIIIEGLSPDVRAIGFPGFGLGNGAGKTTTIRMIVGHMSITAGEIAV 63  
 Db 3 LIEVSNLRKEYNHVAQDVFSVEGEIFGILGPNAGKTTTAVCEICGMKRKRDGGEISV 62  
 QY 64 CGSVKENPEKA--ARHIGAVENPELYKFLTGYNLQOQYARMTKGVTKKKID--EIVEL 119  
 Db 63 MGLDPLKOKDLAELRESIGIQQSELPPKMKVWEALELYSTF-----YRDPVDRRELKID 118  
 QY 120 VGLKNRINDKVITYSLGMRQRLGLAOSLLHDPKLLILDEPTNGLDPAGIREIRDYLRKLT 179  
 Db 119 WGLSDKADTAYGSLSGGQQQRLSIALALVGPRIAVFDELTTALDHPHARRETWKLEKV- 177  
 QY 180 REKGMVIVSSHLLSEMELMCDRIATIQNGKLRDIQHVHG-----PAR 222  
 Db 178 REQDVTVLLVTHFMEAEERLCRIATIESGRVVALDTPSLVSRVDEQQIIRFKPSVPM 237  
 QY 223 DEKKRYIQADDTQALTREAAA-FRKVKYDEAEGGIELSIQKDEVPDLIKHLTDSGVRLYE 282  
 Db 238 DE---LLTSLPEVSVTRSKSQVTVV-----GKGNVYAV-----ISVLARNQIVANE 282  
 QY 283 KVANKSKLEDFLEITADK 301  
 Db 283 LRLEQASLDDAFVALTGSK 301

RESULT 10  
 US-10-449-902-54801  
 ; Sequence 54801, Application US/10449902  
 ; Publication No. US20060123505A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: National Institute of Agrobiological Sciences.  
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.  
 ; APPLICANT: The Institute of Physical and Chemical Research.  
 ; APPLICANT: Foundation for Advancement of International Science.  
 ; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF  
 ; FILE REFERENCE: MOA-A0205Y1-US  
 ; CURRENT APPLICATION NUMBER: US/10/449,902  
 ; CURRENT FILING DATE: 2003-05-29  
 ; PRIOR APPLICATION NUMBER: JP 2002-203269  
 ; PRIOR FILING DATE: 2002-05-30  
 ; PRIOR APPLICATION NUMBER: JP 2002-383870  
 ; PRIOR FILING DATE: 2002-12-11  
 ; NUMBER OF SEQ ID NOS: 56791  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 54801  
 ; LENGTH: 968  
 ; TYPE: PRT  
 ; ORGANISM: Oryza sativa  
 ; ORGANISM: Oryza sativa  
 US-10-449-902-54801

Query Match 20.5%; Score 315.5; DB 6; Length 968;  
 Best Local Similarity 36.3%; Pred. No. 4.1e-14;  
 Matches 73; Conservative 43; Mismatches 76; Indels 9; Gaps 4;  
 QY 20 IEGLSPDVRAIGFPGFGLGNGAGKTTTIRMIVGHMSITAGEIAVCGSVKKE--NFEKAAR 77

Db 549 VKGLWNLEKDLQFLGLSPNGAGKTTTISCLTITGITPTGDMITGHVSRTAGSMNRR 608  
Qy 78 HIGAIVENPELYKFLTCYQNLQOYARMTKGVTKKKIDIVE----LVGLKRNINDKVKTY 133  
Db 609 MIGVCPDFDILMDALTAKERHMFASI-KGLPPSTIKSVABQSILIQVKLSQANVRAGSY 667  
Qy 134 SLGMRORGLAQSLHDPKLLILDEPTNGDPPAGIREIRDYLRKLTREKGMVIVSSHLL 193  
Db 668 SGGMKRLSVAIALIGDPKLVFLDEPTTGMDDPITRRHVWDIIEB--AKKGRAIVLVTTHSM 725  
Qy 194 SEMELMCDRIAIIONGKLRDI 214  
Db 726 BEADILSDRIAINAKGLRCCI 746

## RESULT 11

US-11-293-697-4238  
; Sequence 4238, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cdna  
; FILE REFERENCES: H1-A0106  
; CURRENT APPLICATION NUMBER: US/11/293,697  
; CURRENT FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 4238  
; LENGTH: 815  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-293-697-4238

Query Match 20.4%; Score 314; DB 7; Length 815;  
Best Local Similarity 30.7%; Pred. No. 4.2e-14;  
Matches 96; Conservative 62; Mismatches 115; Indels 40; Gaps 10;

Qy 15 RGKKI-IEGLSPDVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAGEIAVCGSVSKENFE 73  
Db 495 RKKKIARNISFCVQEGEILGLLSPGAGKSSIRMSIGITKPTAGEVELKGC----- 548  
Qy 74 KAARHIGAIVENPELYKFLTCYQNLQOYARMTKGVTKK----KIDEIVELVGLKRNINDX 129  
Db 549 SVLGHGVCQENLWPMPLTREHLEVYAAV-KGLRKADARLAIALVSAFKLHQLNVP 607  
Qy 130 VKTYSLGMRORGLAQSLHDPKLLILDEPTNGDPPAGIREIRDYLRKLTREKGMVIVS 189  
Db 608 VQKLTAGITRKLCLFVLSLGNPSVLLDDEPSTGIDPTGQQMQAQIAQVVKNTERGVLTT 667  
Qy 190 SHLSELMCDRIAIIONGKLR----DIQHVHGADEKKRYI---QADDTQALTRAA 243  
Db 668 THNLAEALCDRAIVMSVSLRIGSIQHL-----KNKLGKGVILELKVETSKVTLVHT 723  
Qy 244 APRKVKVDEA--EGGIELSIQKDEVPD-----IKHLTDSGVPELYEYKAVNKS 289  
Db 724 EILKLPQAAGQERYSLTYKLPVADVPLSQTFHKLKAVK----NFNLEYSLSQCT 779  
Qy 290 LEDRFLEITADKE 302  
Db 780 LEKVFLELSKEQE 792

## RESULT 12

US-11-293-697-2603  
; Sequence 2603, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cdna  
; FILE REFERENCES: H1-A0106  
; CURRENT APPLICATION NUMBER: US/11/293,697

; CURRENT FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2603  
; LENGTH: 559  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-293-697-2603

Query Match 19.7%; Score 303.5; DB 7; Length 559;  
Best Local Similarity 28.9%; Pred. No. 1.4e-13;  
Matches 88; Conservative 73; Mismatches 115; Indels 29; Gaps 10;

Qy 23 LSPDVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAGEIAVCGSVSK-ENFEKAAHIGA 81  
Db 236 ISFCVKKGEILGLLSPGAGKSTIITLVGDIETSGQVFLGDYSSSETSEDDSLKCMGY 295  
Qy 82 IVENPELYKFLTCYQNLQOYARMTKGVY----KKKIDEIVELVGLKRNINDKVKTYSIGM 137  
Db 296 CPQINLWPDPTTLOSHFEIYGAV-KGMSASDMKEVISRITHALDLKHLQKTVKKLPAGI 354  
Qy 138 RQRGLAQSLHDPKLLILDEPTNGDPPAGIREIRDYLRKLTREKGMVIVSSHLLSEME 197  
Db 355 KRKLCFALSMLGNPQITLLDEPSTGMDPKAKQHMWRAIRTAFAKVRKRAAILTTHYMBEAE 414  
Qy 198 LMCORIAIIONGKLR----DIQHV-----HGADEKKRYIYIQADDTQALTRAA-APRKV 248  
Db 415 AVCDRVAIVMSVSLRIGSIQHLKSKFGKGYPLKIKLMDWLENLEVDRLQREIQVIFPNA 474  
Qy 249 KVDEAEGGIELSIQKDEVP-DLTKHLTDSGVRLYEYK---AVNK-----SLEDRFLEIT 298  
Db 475 SROESFS-----SILAHKIPKEDVQSLSQSPFKLEEAHFAIBESFSQATLEQVVFVELT 530  
Qy 299 ADKEE 303  
Db 531 KEQEE 535

## RESULT 13

US-10-471-571A-3086  
; Sequence 3086, Application US/10471571A  
; Publication No. US20060115490A1  
; GENERAL INFORMATION:  
; APPLICANT: CHIRON SpA  
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS  
; FILE REFERENCE: P026927W0  
; CURRENT APPLICATION NUMBER: US/10/471,571A  
; CURRENT FILING DATE: 2003-09-12  
; PRIOR APPLICATION NUMBER: GB-0107661.1  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 5642  
; SOFTWARE: SeqWin99, version 1.03  
; SEQ ID NO 3086  
; LENGTH: 325  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)-(325)  
; OTHER INFORMATION: hypothetical protein  
US-10-471-571A-3086

Query Match 19.6%; Score 301.5; DB 6; Length 325;  
Best Local Similarity 27.2%; Pred. No. 9.2e-14;  
Matches 89; Conservative 72; Mismatches 139; Indels 27; Gaps 9;

Qy 4 LLELKNVSKTIRKGIIEGLSFDVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAGIAV 63  
Db 1 VIKPKVTKRYGKHVAVDNISFNINEGEPFVLGPGSGCGKTTTLKMINRLIHSEGIYF 60  
Qy 64 CGVSVKENFEKAAR-HIGAIVENPELYKFLTCYQNLQOYARMTKGVTK---KKIDEIVEL 119

```
Db      61 KDRPISDPYVYEMRWIDGYVLOQIALFPHTIKENIAQVPQMKWKEKDIDKRVDELLEM 120
Qy      120 VGL-----KQRINDKVTYSLGMRORLGLAQSLHDPKLLILDEPTNGLDPAQIRIDY 174
Db      121 VGLPEKYNKRPDEL---SGGQRQVGVIRALAADPPVILMDPEFVSALDPTISREKLQDD 177
Qy      175 LRKLTRKGMNAVIVSSHLLSEMELMCDRIAIQNGKLRDIOHVHGPARDEKRYIYIQ--- 231
Db      178 LIELQTKIKKTIIFVTHDIOEAMKLGDKICLLNEGHEIQIDTPEGFKNNPQSEFVKQFMG 237
Qy      232 --ADDDQALTRAAAFKRV---KVDEAEGGIELSIQKDEVP-DLIKHLTDSGVRLYEVK 284
Db      238 SHLEDDAPCVENAIIRDIDIMKPIDEVITSMSPYIVQNPQIEVLYQLLSSESRVIMVQ 297
Qy      285 --AVNKSLEDR---FLEITADKEEAQH 306
Db      298 EDSVGQYVIDRDKIDFKYLSOKKEVAQH 324
```

## RESULT 14

```
US-10-471-571A-2868
; Sequence 2868, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927W0
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 2868
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(341)
; OTHER INFORMATION: ABC transporter ATP-binding
US-10-471-571A-2868
```

```
Query Match      19.2%; Score 296.5; DB 6; Length 341;
Best Local Similarity 30.4%; Pred. No. 2.2e-13;
Matches 73; Conservative 55; Mismatches 97; Indels 15; Gaps 4;

Qy      4 LLELKNVSKTIRGKK----IIEGLSFDVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAG 59
Db      1 VIELKEVVKYRTKNKEVLAVDHVNLISIRAGSIYGVIGFSGAGKSTLIRMFNHLAPTS 60
Qy      60 EIAVCGVSV---KENFEKAARHIGAIVENPELYKFLTGYNLQ---QYARMTKGVTKKK 112
Db      61 EVIIDGHIQGLSKNGRLAKRQKQVSMIFQHFNLWSRTVLKNI MFLEIAGVPRRAKQK 120
Qy      113 IDEIVELVGLKRNINDKVTYSLGMRORLGLAQSLHDPKLLILDEPTNGLDPAQIRIR 172
Db      121 ALELVELVGLKRGREKAYPSELGGQKQKQVGIARALANDPTVLLCDEATSA LDPQTDEIL 180
Qy      173 DYLRKLTREKGMNAVIVSSHLLSEMELMCDRIAIQNGKLRD----IQHVHGPARDEKRY 228
Db      181 DLLLLKIREQNLTVLITHEMHVIRRICDEVAVMSESGKVI EQGPVTQVPENPQHTVTKRF 240
```

## RESULT 15

```
US-10-471-571A-678
; Sequence 678, Application US/10471571A
; Publication No. US20060115490A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE: P026927W0
```

```
; CURRENT APPLICATION NUMBER: US/10/471,571A
; CURRENT FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: GB-0107661.1
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 5642
; SOFTWARE: SeqWin99, version 1.03
; SEQ ID NO 678
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(256)
; OTHER INFORMATION: ABC transporter ecsA
US-10-471-571A-678
```

```
Query Match      19.1%; Score 294; DB 6; Length 256;
Best Local Similarity 28.5%; Pred. No. 2.2e-13;
Matches 68; Conservative 62; Mismatches 87; Indels 22; Gaps 5;

Qy      16 GK-KIIEGLSFDVRAGEIFGFLGPNAGKTTTIRMIVGHMSITAGIACVGVKVENFEK 74
Db      23 GKRPVIKIDINFELNKGELVGLIGLNGAGKSTTIKHMGLLTPMEGSLISDINDDIEA 82
Qy      75 AARHIGAIVENPELYKFLTGYNLQYARMT-----KGVTKKKIDEIVELVGLKNRIN 127
Db      83 YRRKLSYIPESPVIYEELT----LESHIEMTAWAYDIDRDETNRAMPPLDKTRLENELK 138
Qy      128 DKVKTYSLGMRORLGLAQSLHDPKLLILDEPTNGLDPAQIRIRDYLRKLTREKGMNAV 187
Db      139 VPFSEFSKGMKQKVMICAFIVNPELYIIDEPLGLDPLGLIQSLMDLMVE-KKNEGRTVL 197
Qy      188 VSHLLSEMELMCDRIAIQNGK-----LRDIQHVHGPARDEKRYIYIQADDTQA 237
Db      198 MSTHILATAERYCDREFIILDEGEVWAFGDLEALRQQTGLHNTLDDIYIHVTOGGDVHA 256
```

Search completed: July 13, 2006, 13:54:27  
Job time : 30 secs